GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 21, 2005, 08:04:52 ; Search time 83 Seconds
(without alignments)
69.153 Million cell updates/sec

Title: US-09-845-765-1
Perfect score: 83
Sequence: 1 ADSGEGDFLAEGGGVR 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	83	100.0	16	2	AAR96194	Aar96194 Fibrinoge
2	83	100.0	16	2	AAW04619	Aaw04619 Fibrinope
3	83	100.0	16	2	AAY57487	Aay57487 Antimicro
4	83	100.0	16	4	ABB56219	Abb56219 Vascular
5	83	100.0	16	4	AAB91959	Aab91959 Fibronect
6	83	100.0	16	4	ABB52337	Abb52337 Human API
7	83	100.0	16	5	ABG73668	Abg73668 Linear HI
8	83	100.0	16	5	ABG78799	Abg78799 Multiple
9	83	100.0	16	5	ABG70000	Abg70000 Antimicro
10	83	100.0	16	5	ABG69911	Abg69911 Rabbit pl
11	83	100.0	16	6	ABP60019	Abp60019 Biopolyme
12	83	100.0	16	6	ABP60640	Abp60640 Fibrinope
13	83	100.0	16	6	ADA18542	Ada18542 Human alp
14	83	100.0	16	6	ABR58740	Abr58740 Alzheimer
15	83	100.0	16	7	ADF51340	Adf51340 Antiangio
16	83	100.0	16	7	ADK41579	Adk41579 Human fib
17	83	100.0	16	8	ADF90108	Adf90108 Human fib
18	83	100.0	16	8	ADN31682	Adn31682 Human Alz
19	83	100.0	16	8	ADQ96599	Adq96599 Human alp
20	83	100.0	17	4	AAB91960	Aab91960 Fibronect
21	83	100.0	17	6	ABU08833	Abu08833 Alpha fib
22	83	100.0	17	6	ABU09101	Abu09101 Alpha fib
23	83	100.0	17	8	ADG93163	Adg93163 Novel exp
24	83	100.0	17	8	ADJ65841	Adj65841 Fibrinope
25	83	100.0	17	8	ADN03327	Adn03327 Exemplary
26	83	100.0	18	2	AAR96193	Aar96193 Fibrinoge
27	83	100.0	18	6	ABU08834	Abu08834 Alpha fib
28	83	100.0	18	6	ABU08837	Abu08837 Alpha fib
29	83	100.0	18	6	ADA18541	Ada18541 Human alp
30	83	100.0	19	2	AAR96192	Aar96192 Fibrinoge
31	83	100.0	20	2	AAR96191	Aar96191 Fibrinoge
32	83	100.0	20	2	AAY57488	Aay57488 Antimicro
33	83	100.0	20	5	ABG69912	Abg69912 Rabbit pl
34	83	100.0	21	2	AAR96183	Aar96183 Fibrinoge
35	83	100.0	22	1	AAP90276	Aap90276 Antigen p
36	83	100.0	22	2	AAR96190	Aar96190 Fibrinoge
37	83	100.0	22	2	AAR96182	Aar96182 Fibrinoge
38	83	100.0	24	5	AAO21114	Aao21114 Anti-angi
39	83	100.0	24	5	AAO21113	Aao21113 Anti-angi
40	83	100.0	24	5	AAO21112	Aao21112 Anti-angi
41	83	100.0	24	5	AAO21115	Aao21115 Anti-angi
42	83	100.0	24	6	AAO27090	Aao27090 Fibrinoge
43	83	100.0	24	6	AAO27097	Aao27097 Fibrinoge
44	83	100.0	24	7	ADF51362	Adf51362 Antiangio
45	83	100.0	24	7	ADF51327	Adf51327 Antiangio

ALIGNMENTS

RESULT 1
AAR96194
ID AAR96194 standard; peptide; 16 AA.
XX
AC AAR96194;
XX
DT 19-DEC-1996 (first entry)
XX
DE Fibrinogen epitope probe, represents alpha chain residues 1-16.
XX
KW Epitope; cleavage product; human; leukocyte elastase; HLE; fibrinogen;
KW monoclonal antibody; probe; detection; antigen; blood; peritoneal fluid;
KW sputum; broncheoalveolar lavage fluid; assay; inhibitor; arthritis;
KW pulmonary emphysema; chronic bronchitis; cystic fibrosis; bronchiectasis;
KW chronic obstructive pulmonary disease; myelogenous leukaemia;
KW infantile respiratory distress syndrome; gout;
KW adult respiratory distress syndrome.
XX
OS Homo sapiens.
XX
PN WO9614580-A1.
XX
PD 17-MAY-1996.
XX
PF 03-NOV-1995; 95WO-US013794.
XX
PR 07-NOV-1994; 94US-00335524.
PR 06-JUN-1995; 95US-00469141.
XX
PA (MERI) MERCK & CO INC.
XX
PI Mumford RA, Davies DTP, Dahlgren ME, Boger JS, Humes JL;
XX
DR WPI; 1996-251888/25.
XX
PT New isolated fibrinogen derived cleavage products - used for detection of
PT leukocyte elastase activity in disease diagnosis and for evaluating
PT elastase inhibitors.
XX
PS Example 5; Page 42; 109pp; English.
XX
CC The sequences given in AAR96182-94 represent antigenic probes derived
CC from the first 21 amino acids of human fibrinogen. These probes are used
CC to determine antibody titre against other fibrinogen cleavage products.
CC The monospecific antibodies may be used to assay for the formation of
CC complimentary cleavage product antigens or epitopes in whole blood or
CC other body fluids, peritoneal fluid, sputum or broncheoalveolar lavage
CC fluid. The assay for cleavage products is dependent upon the presence of

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CC   HLE in the sample. This assay can also be used for the evaluation of HLE
CC   inhibitors. The antibodies may be used to diagnose and monitor diseases
CC   such as arthritis, gout, pulmonary emphysema, chronic bronchitis, cystic
CC   fibrosis, chronic obstructive pulmonary disease, bronchiectasis, adult or
CC   infantile respiratory distress syndrome and myelogenous leukaemia. See
CC   also AAR96146-81
XX
SQ   Sequence 16 AA;

  Query Match             100.0%;  Score 83;  DB 2;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ADSGEGDFLAEGGGVR 16
              ||||||||||||||||
Db          1 ADSGEGDFLAEGGGVR 16


RESULT 2
AAW04619
ID   AAW04619 standard; peptide; 16 AA.
XX
AC   AAW04619;
XX
DT   13-AUG-1997  (first entry)
XX
DE   Fibrinopeptide A peptide for mass spectrometry analysis.
XX
KW   Mass spectrometry; polymer analysis; biopolymer analysis.
XX
OS   Synthetic.
XX
PN   WO9636986-A1.
XX
PD   21-NOV-1996.
XX
PF   17-MAY-1996;   96WO-US007146.
XX
PR   19-MAY-1995;   95US-00446055.
PR   19-MAY-1995;   95US-00447175.
XX
PA   (PERS-) PERSEPTIVE BIOSYSTEMS INC.
XX
PI   Patterson DH,  Tarr GE;
XX
DR   WPI; 1997-012308/01.
XX
PT   Sequencing polymers, e.g. DNA, RNA, peptide nucleic acids, proteins, etc.
PT   - by obtaining mass to charge ratios of polymer fragments, pref. using
PT   mass spectrometer, and performing statistical analysis.
XX
PS   Example 2; Page 32; 86pp; English.
XX
CC   A method of obtaining sequence information about a polymer (e.g. DNA,
CC   RNA, peptide nucleic acids, proteins, peptides and carbohydrates)
CC   comprising monomers of known mass has been claimed. The present sequence
CC   represents a fibrinopeptide A peptide, and was used as an example as a
CC   digestion before analysis by mass spectrometry, using this novel on-plate
CC   strategy. Total sequence information from a nine well digestion can be
CC   represented in a single digestion or it is often derived from two or more
CC   wells. The methods, apparatus and kit (claimed) can be used for the
CC   analysis of polymers, particularly biopolymers, e.g. DNA, RNA, peptide
CC   nucleic acids, proteins, peptides and carbohydrates. It provides a rapid,
CC   automated and cost effective sequencing of polymers, with a statistical
CC   certainty
XX
SQ   Sequence 16 AA;

  Query Match             100.0%;  Score 83;  DB 2;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ADSGEGDFLAEGGGVR 16
              ||||||||||||||||
Db          1 ADSGEGDFLAEGGGVR 16


RESULT 3
AAY57487
ID   AAY57487 standard; peptide; 16 AA.
XX
AC   AAY57487;
XX
DT   25-FEB-2000  (first entry)
XX
DE   Antimicrobial peptide CS-FBP-alpha SEQ ID NO:25.
XX
KW   Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
KW   antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX
OS   Synthetic.
OS   Oryctolagus cuniculus.
XX
PN   WO9942119-A1.
XX
PD   26-AUG-1999.
XX
PF   17-FEB-1999;   99WO-US003350.
XX
PR   18-FEB-1998;   98US-00025319.
XX
PA   (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
PI   Yeaman MR,  Shen AJ;
XX
DR   WPI; 1999-527417/44.
XX
PT   Antimicrobial peptides for potentiating antimicrobial agents active
PT   against bacteria and fungi.
XX
PS   Disclosure; Page 120; 166pp; English.
XX
CC   The present invention describes an antimicrobial peptide (AP) for direct
CC   activity or for potentiating antimicrobial agents active against
CC   organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC   containing an amino acid sequence selected from the group consisting
CC   essentially of a first peptide template XZBZBXBXB and its derivatives
CC   selected from XZBBZBXBXB, BXZXB, BXZXZXB, XBBXZXBBX and BBXZBBXZ; and (b)
CC   a second peptide template XBBXX and their derivatives selected from the
CC   group consisting of XBBXBBX, XBBXXBBX, BXXBXXB, XBBZXXBB, and
CC   XBBZXXBBXXZBBX; where B = at least one positively charged amino acid; X =
CC   at least one non-polar hydrophobic amino acid; Z = at least one aromatic
CC   amino acid, and where B, X and Z may be separated by one or more other
CC   amino acids. The peptides can be used to treat bacterial and fungal
CC   infections. The peptides also increase the antimicrobial activity of
CC   neutrophils. The peptides overall effect cellular disruption and rapid
CC   apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
CC   used in the exemplification of the present invention
XX
SQ   Sequence 16 AA;

  Query Match             100.0%;  Score 83;  DB 2;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ADSGEGDFLAEGGGVR 16
              ||||||||||||||||
Db          1 ADSGEGDFLAEGGGVR 16


RESULT 4
ABB56219
ID   ABB56219 standard; peptide; 16 AA.
XX
AC   ABB56219;
XX
```

DT 15-FEB-2002 (first entry)
XX
DE Vascular dementia-associated protein isoform (VPI) 419.
XX
KW Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;
KW diagnosis; prognosis; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200169261-A2.
XX
PD 20-SEP-2001.
XX
PF 14-MAR-2001; 2001WO-GB001106.
XX
PR 15-MAR-2000; 2000GB-00006285.
PR 24-NOV-2000; 2000GB-00028734.
PR 28-NOV-2000; 2000US-00724391.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Herath HMAC, Parekh RB, Rohlff C;
XX
DR WPI; 2001-557937/62.
XX
PT Screening, diagnosis or prognosis of vascular dementia (VD), useful for
PT determining stage of VD and monitoring the effect of VD therapy,
PT comprises analyzing body fluid by 2-dimensional electrophoresis for
PT features correlated with VD.
XX
PS Claim 6; Page 39; 151pp; English.
XX
CC The invention relates to screening, diagnosis or prognosis of Vascular
CC Dementia (VD) in a subject comprising analysing body fluid from the
CC subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of
CC features containing at least one chosen feature whose relative abundance
CC correlates with the presence, absence, stage or severity of VD or
CC predicts the onset or course of VD, especially detecting in a sample of
CC cerebrospinal fluid (CSF) from the subject one of 223 VD-associated
CC protein isoforms (VPIs) (ABB55801-ABB56295) as fully defined in the
CC specification. Detecting VD-associated features and VPI is useful for the
CC screening, diagnosis or prognosis of VD, for determining the stage or
CC severity of VD, for identifying a subject at risk of VD or for monitoring
CC the effect of therapy administered to a subject having VD. Nucleic acids
CC encoding a VPI or inhibiting the function of a VPI are useful for the
CC treatment of VD and for gene therapy
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 83; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSGEGDFLAEGGGVR 16
||||||||||||||||
Db 1 ADSGEGDFLAEGGGVR 16

RESULT 5
AAB91959
ID AAB91959 standard; peptide; 16 AA.
XX
AC AAB91959;
XX
DT 22-JUN-2001 (first entry)
XX
DE Fibronectin fragment and fibrin related peptide SEQ ID NO:1135.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US013576.
XX
PR 17-MAY-1999; 99US-0134406P.
PR 10-SEP-1999; 99US-0153406P.
PR 15-OCT-1999; 99US-0159783P.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX
DR WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity.
XX
PS Disclosure; Page 567; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity in
CC vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 83; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSGEGDFLAEGGGVR 16
||||||||||||||||
Db 1 ADSGEGDFLAEGGGVR 16

RESULT 6
ABB52337
ID ABB52337 standard; peptide; 16 AA.
XX
AC ABB52337;
XX
DT 08-FEB-2002 (first entry)
XX
DE Human API-118 tryptic digest peptide #2.
XX
KW Human; neuroprotective; nootropic; gene therapy; vaccine;
KW Alzheimer's disease; Alzheimer's Disease-Associated Feature; AF;
KW Alzheimer's Disease-Associated Protein Isoform; API; tryptic digest;
KW Expression Reference Protein Isoform; ERPI; proteolysis.
XX
OS Homo sapiens.
XX
PN WO200175454-A2.
XX
PD 11-OCT-2001.
XX

PF 03-APR-2001; 2001WO-US010908.
XX
PR 03-APR-2000; 2000US-0194504P.
PR 28-NOV-2000; 2000US-0253647P.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
PA (PFIZ) PFIZER INC.
XX
PI Durham KL, Friedman DL, Herath HMAC, Kimmel LH, Parekh RB;
PI Potter DM, Rohlff C, Silber BM, Stiger TR, Sunderland PT;
PI Townsend RR, White F, Williams SA;
XX
DR WPI; 2001-639384/73.
XX
PT Screening for Alzheimer's disease in a mammal, by making two-dimensional
PT array of a feature whose relative abundance correlates with disease, and
PT comparing with abundance of the feature in samples of healthy persons.
XX
PS Example; Page 33; 162pp; English.
XX
CC The invention relates to methods for the screening, diagnosis and
CC prognosis of Alzheimer's disease. The methods involve the detection of
CC Alzheimer's Disease-Associated Features (AFs) and Alzheimer's Disease-
CC Associated Protein Isoforms (APIs) in cerebrospinal fluid, serum or
CC plasma. The abundance of the AFs and APIs is then normalised to an
CC Expression Reference Protein Isoform (ERPI) in order to determine whether
CC a patient is suffering from, or has a predisposition to, Alzheimer's
CC Disease. The relative abundance of the AFs and APIs correlates with the
CC severity of Alzheimer's Disease. The present sequence is a peptide
CC produced from an API by proteolysis
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 83; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSGEGDFLAEGGGVR 16
||||||||||||||||
Db 1 ADSGEGDFLAEGGGVR 16

RESULT 7
ABG73668
ID ABG73668 standard; peptide; 16 AA.
XX
AC ABG73668;
XX
DT 11-MAR-2003 (first entry)
XX
DE Linear HIV-1 gp120 V3-loop derived peptide ligand SEQ ID 11.
XX
KW gp120; interaction; co-receptor; CXCR4; CCR5; refractive index; V3 loop;
KW 7-helix transmembrane receptor; glycopeptide; virucide; anti-HIV;
KW HIV infection.
XX
OS Human immunodeficiency virus 1.
OS Synthetic.
XX
PN DE10113042-A1.
XX
PD 26-SEP-2002.
XX
PF 09-MAR-2001; 2001DE-01013042.
XX
PR 09-MAR-2001; 2001DE-01013042.
XX
PA (NOCH-) NOCHT INST TROPENMEDIZIN BERNHARD.
XX
PI Schreiber M, Seifert A, Meyer B;
XX
DR WPI; 2002-752120/82.
XX
PT Identifying compounds that modify interaction of gp120 and co-receptors,
PT useful potentially for treating human immune deficiency virus infection,
PT also new peptides.
XX
PS Claim 10; Page 56; 68pp; German.
XX
CC This invention describes novel substances that modify the interaction
CC between the gp120 protein of human immunodeficiency virus (HIV), or its
CC fragments, with the co-receptors CXCR4, CCR5 and/or other 7-helix
CC transmembrane receptors for HIV. The method comprises (a) immobilizing a
CC ligand for the co-receptor on a gold surface; (b) contacting the ligand
CC with suspended cells that express the co-receptor; and (c) determining
CC interaction by measuring the refractive index (RI) by plasmon resonance.
CC The procedure is repeated using cells that have been incubated with a
CC test compound, and this is identified if RI is lower for cells
CC preincubated with it. The ligand is a linear or cyclic (glyco)peptide
CC that includes the amino acid sequence of an HIV V3 loop (including
CC flanking Cys). The products of the invention have virucide and anti-HIV
CC (human immunodeficiency virus) activity and are useful for prevention
CC and/or treatment of HIV infection. This sequence represents a linear HIV-
CC 1 gp120 V3-loop derived peptide ligand described in the disclosure of the
CC invention
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 83; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSGEGDFLAEGGGVR 16
||||||||||||||||
Db 1 ADSGEGDFLAEGGGVR 16

RESULT 8
ABG78799
ID ABG78799 standard; peptide; 16 AA.
XX
AC ABG78799;
XX
DT 29-NOV-2002 (first entry)
XX
DE Multiple sclerosis associated feature (MSF) tryptic digest peptide #287.
XX
KW Multiple sclerosis; MS; multiple sclerosis associated feature; MSAF;
KW human; multiple sclerosis-associated protein isoform; MSPI;
KW antiinflammatory; neuroprotective.
XX
OS Homo sapiens.
XX
PN WO200259604-A2.
XX
PD 01-AUG-2002.
XX
PF 25-JAN-2002; 2002WO-GB000330.
XX
PR 26-JAN-2001; 2001US-0264404P.
PR 20-NOV-2001; 2001US-0331647P.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Herath HMAC, Parekh RB, Rohlff C;
XX
DR WPI; 2002-599812/64.
XX
PT Screening or diagnosing multiple sclerosis (MS), useful for e.g.
PT determining the stage or severity of MS, comprises detecting the presence
PT of MS-associated features or protein isoforms by 2-dimensional
PT electrophoresis.
XX
PS Disclosure; Page 32; 128pp; English.
XX
CC This invention relates to a novel method for screening or diagnosing

CC multiple sclerosis (MS) in a subject to determine the stage or severity
CC of MS, to identify a subject at risk of developing MS or to monitor the
CC effect of a therapy administered. The method comprises analysing a sample
CC body fluid from the subject by two-dimensional electrophoresis and
CC detecting the presence of multiple sclerosis-associated features (MSFs),
CC or multiple sclerosis-associated protein isoforms (MSPIs). The MSF's of
CC the invention correspond to spots identified on a 2D gel these proteins
CC may have antiinflammatory or neuroprotective activity. The methods of the
CC invention and the compositions are useful for clinical screening,
CC diagnosis and treatment of MS, for monitoring the effectiveness of MS
CC treatment, for selecting participants in clinical trials, for identifying
CC patients most likely to respond to a particular therapeutic treatment and
CC for screening and developing drugs for treatment of MS. Agents that
CC modulate the expression or activity of an MSPI are useful for treating
CC MS, for preventing or delaying the onset or development of MS, to prevent
CC or delay the progression of MS, or to ameliorate the symptoms MS. Nucleic
CC acids comprising a sequence encoding an MSPI, MSPI-related polypeptide,
CC or their fragments are useful for promoting MSPI function by gene
CC therapy. The present sequence represents a human multiple sclerosis
CC associated feature tryptic digest peptide of the invention
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 83; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSGEGDFLAEGGGVR 16
||||||||||||||||
Db 1 ADSGEGDFLAEGGGVR 16

RESULT 9
ABG70000
ID ABG70000 standard; peptide; 16 AA.
XX
AC ABG70000;
XX
DT 21-OCT-2002 (first entry)
XX
DE Antimicrobial peptide CS-FBPa.
XX
KW Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2;
KW bacterial infection; fungal infection; fungicide; disinfectant;
KW preservative; foods; cosmetic; multiple antibiotic resistance.
XX
OS Unidentified.
XX
PN WO200255554-A2.
XX
PD 18-JUL-2002.
XX
PF 24-AUG-2001; 2001WO-US041877.
XX
PR 25-AUG-2000; 2000US-00648816.
XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
PI Yeaman MR, Shen AJ;
XX
DR WPI; 2002-590659/63.
XX
PT New antimicrobial peptide composition for the prevention and treatment of
PT infections caused by organisms, such as bacteria and fungi, exhibiting
PT multiple antibiotic resistance.
XX
PS Disclosure; Page 18; 221pp; English.
XX
CC The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbiocidal protein), and retromers,
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC or for potentiating antimicrobial agents active against organisms such as
CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations of the peptides described above,
CC and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is an antimicrobial peptide detailed in the
CC disclosure but specifically excluded from the scope of the invention
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 83; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSGEGDFLAEGGGVR 16
||||||||||||||||
Db 1 ADSGEGDFLAEGGGVR 16

RESULT 10
ABG69911
ID ABG69911 standard; peptide; 16 AA.
XX
AC ABG69911;
XX
DT 21-OCT-2002 (first entry)
XX
DE Rabbit platelet microbicidal protein, PMP-2, based peptide #23.
XX
KW Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2;
KW bacterial infection; fungal infection; fungicide; disinfectant;
KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
KW mutant; mutein.
XX
OS Oryctolagus cuniculus.
OS Synthetic.
XX
PN WO200255554-A2.
XX
PD 18-JUL-2002.
XX
PF 24-AUG-2001; 2001WO-US041877.
XX
PR 25-AUG-2000; 2000US-00648816.
XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
PI Yeaman MR, Shen AJ;
XX
DR WPI; 2002-590659/63.
XX
PT New antimicrobial peptide composition for the prevention and treatment of
PT infections caused by organisms, such as bacteria and fungi, exhibiting
PT multiple antibiotic resistance.
XX
PS Disclosure; Page 135; 221pp; English.

XX
CC The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbiocidal protein), and retromers,
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC or for potentiating antimicrobial agents active against organisms such as
CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations of the peptides described above,
CC and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 83; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSGEGDFLAEGGGVR 16
||||||||||||||||
Db 1 ADSGEGDFLAEGGGVR 16

RESULT 11
ABP60019
ID ABP60019 standard; peptide; 16 AA.
XX
AC ABP60019;
XX
DT 24-FEB-2003 (first entry)
XX
DE Biopolymer disease specific marker.
XX
KW Biopolymer; disease specific marker; marker; myocardial infarction;
KW alpha fibrinogen.
XX
OS Homo sapiens.
XX
PN WO200288716-A2.
XX
PD 07-NOV-2002.
XX
PF 25-APR-2002; 2002WO-CA000577.
XX
PR 30-APR-2001; 2001US-00845765.
XX
PA (SYNX-) SYN.X PHARMA INC.
XX
PI Jackowski G, Thatcher B, Marshall J, Yantha J, Vrees T;
XX
DR WPI; 2003-111905/10.
XX
PT New biopolymer marker or its analyte, useful for determining the presence
PT or absence of at least one particular disease state, such as myocardial
PT infarction.
XX
PS Claim 1; Page 28; 28pp; English.
XX
CC The invention relates to a biopolymer disease specific marker. The
CC biopolymer marker is useful in indicating at least one particular disease
CC state, such as myocardial infarction. The method is useful for evidencing
CC and categorising at least one biopolymer marker sequence to determine the
CC presence or absence of at least one disease state. This marker is
CC characterised as an alpha fibrinogen having a molecular weight of 1518
CC daltons. The current sequence represents the biopolymer disease specific
CC marker of the invention
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 83; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSGEGDFLAEGGGVR 16
||||||||||||||||
Db 1 ADSGEGDFLAEGGGVR 16

RESULT 12
ABP60640
ID ABP60640 standard; peptide; 16 AA.
XX
AC ABP60640;
XX
DT 28-MAR-2003 (first entry)
XX
DE Fibrinopeptide A.
XX
KW Fibrinopeptide A; N-terminus; protein identification.
XX
OS Unidentified.
XX
PN WO200295419-A2.
XX
PD 28-NOV-2002.
XX
PF 20-MAY-2002; 2002WO-US016247.
XX
PR 23-MAY-2001; 2001US-00863786.
PR 20-DEC-2001; 2001US-0343019P.
XX
PA (AMSH) AMERSHAM BIOSCIENCES AB.
PA (PROC) PROCTER & GAMBLE CO.
XX
PI Bhikhabhai R, Liminga M, Maloisel J, Palmgren R, Keough TW;
PI Youngquist RS, Vaughn HL, Yelm KE;
XX
DR WPI; 2003-175111/17.
XX
PT Identification of polypeptide useful in proteomics, involves
PT derivatizating N-terminus or N-termini of polypeptide with acidic reagent
PT containing sulfonyl or sulfonic acid moiety coupled to activated ester
PT moiety.
XX
PS Example 3; Page 29; 90pp; English.
XX
CC The invention relates to a novel method for the identification of a
CC polypeptide involving a step of derivatising the N-terminus of the
CC polypeptide or the N-termini of one or more polypeptides with acidic
CC reagent containing a sulfonyl or sulfonic acid moiety coupled to an
CC activated ester moiety, analysing the derivative using mass spectrometry
CC and interpreting the resulting fragmentation pattern. The present
CC sequence represents Fibrinopeptide A, used in example 3 of the invention
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 83; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;

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  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ADSGEGDFLAEGGGVR 16
              ||||||||||||||||
Db          1 ADSGEGDFLAEGGGVR 16


RESULT 13
ADA18542
ID   ADA18542 standard; peptide; 16 AA.
XX
AC   ADA18542;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human alpha fibrinogen peptide #2.
XX
KW   Alpha fibrinogen; human; myocardial infarction; SELDI; mass spectrometry;
KW   surfaces enhanced for laser desorption/ionisation.
XX
OS   Homo sapiens.
XX
PN   US2002160423-A1.
XX
PD   31-OCT-2002.
XX
PF   30-APR-2001; 2001US-00846780.
XX
PR   30-APR-2001; 2001US-00846780.
XX
PA   (JACK/) JACKOWSKI G.
PA   (THAT/) THATCHER B.
PA   (MARS/) MARSHALL J.
PA   (YANT/) YANTHA J.
PA   (VREE/) VREES T.
XX
PI   Jackowski G,  Thatcher B,  Marshall J,  Yantha J,  Vrees T;
XX
DR   WPI; 2003-219987/21.
XX
PT   Biopolymer marker useful in indicating particular disease state
PT   particularly myocardial infarction.
XX
PS   Claim 1; Page 7; 10pp; English.
XX
CC   The invention relates to a biopolymer marker useful in indicating at
CC   least one particular disease state. This marker is characterised as alpha
CC   fibrinogen having a molecular weight of 1536 Daltons and is useful for
CC   indicating a disease state, in particular myocardial infarction. The
CC   marker sequences are useful as antigens in immunoassays for the detection
CC   of those individuals suffering from the disease known to be evidenced by
CC   the marker sequence. The marker provides an efficient diagnostic tool for
CC   rapidly and accurately diagnosing disease states such as myocardial
CC   infarction. The marker was detected by the technique of surfaces enhanced
CC   for laser desorption/ionisation (SELDI) mass spectroscopy. The present
CC   sequence is the alpha fibrinogen marker peptide.
XX
SQ   Sequence 16 AA;

  Query Match             100.0%;  Score 83;  DB 6;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ADSGEGDFLAEGGGVR 16
              ||||||||||||||||
Db          1 ADSGEGDFLAEGGGVR 16


RESULT 14
ABR58740
ID   ABR58740 standard; peptide; 16 AA.
XX
AC   ABR58740;
XX
DT   11-JUL-2003  (first entry)
XX
DE   Alzheimer's Disease-associated protein isoform, API-378, SEQ ID 8.
XX
KW   Nootropic; Neuroprotective; Alzheimer's disease; API; human;
KW   Alzheimer's Disease-associated protein isoform.
XX
OS   Homo sapiens.
XX
PN   WO2003028543-A2.
XX
PD   10-APR-2003.
XX
PF   03-OCT-2002; 2002WO-US031642.
XX
PR   03-OCT-2001; 2001US-0326708P.
XX
PA   (PFIZ ) PFIZER PROD INC.
PA   (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI   Durham LK,  Friedman DL,  Herath HMAC,  Kimmel LH,  Parekh RB;
PI   Potter DM,  Rohlff C,  Silber BM,  Snyder PJ,  Soares HD,  Stiger TR;
PI   Sunderland PT,  Townsend RR,  White WF,  Williams SA;
XX
DR   WPI; 2003-371957/35.
XX
PT   Screening or diagnosing of Alzheimer's disease (AD) determine the stage
PT   or severity of AD in a subject, comprises analyzing a test sample of body
PT   fluid from the subject by 2-dimensional electrophoresis.
XX
PS   Claim 2; Page 31; 179pp; English.
XX
CC   The present invention relates to methods for screening or diagnosing
CC   Alzheimer's disease (AD) to determine the stage or severity of AD in a
CC   subject, to identify subject at risk of developing AD, or to monitor the
CC   effect of therapy administered. The methods comprise analysing a test
CC   sample of body fluid by 2-dimensional electrophoresis to generate a 2-
CC   dimensional array of AD-associated features (AFs). The method
CC   alternatively comprises quantitatively detecting in a sample of body
CC   fluid from the subject, one or more AD-associated protein isoforms (APIs;
CC   ABR58710-ABR59184)
XX
SQ   Sequence 16 AA;

  Query Match             100.0%;  Score 83;  DB 6;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ADSGEGDFLAEGGGVR 16
              ||||||||||||||||
Db          1 ADSGEGDFLAEGGGVR 16


RESULT 15
ADF51340
ID   ADF51340 standard; peptide; 16 AA.
XX
AC   ADF51340;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Antiangiogenic fibrinogen derived peptide 66.
XX
KW   fibrinogen; antiangiogenic; cytostatic; angiogenesis; gene therapy;
KW   cancer; human; mutant; mutein.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "N-terminal acetyl"
```

FT Modified-site 16
FT /note= "C-terminal amide"
XX
PN WO2003070769-A2.
XX
PD 28-AUG-2003.
XX
PF 19-FEB-2003; 2003WO-EP001698.
XX
PR 19-FEB-2002; 2002GB-00003882.
PR 19-FEB-2002; 2002GB-00003883.
PR 23-JUL-2002; 2002GB-00017067.
XX
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS PHARMA GMBH.
PA (BIOA-) BIOACTA LTD.
XX
PI Garcia-Echeverria C, Lewis C, Robinson J;
XX
DR WPI; 2003-731548/69.
XX
PT New polypeptide derived from fibrinogen and having anti-angiogenic
PT activity, useful for preparing a composition for treating cancer.
XX
PS Example 37; Fig 3; 66pp; English.
XX
CC This invention relates to a novel polypeptide derived from fibrinogen
CC comprising 15 or less amino acids which has antiangiogenic activity. The
CC invention may be useful for the development of compounds with a
CC cytostatic activity through the inhibition of angiogenesis. The sequences
CC of the invention may be useful for gene therapy. The polypeptide is
CC useful for inhibiting angiogenesis and in preparing a composition for
CC treating cancer.
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 83; DB 7; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSGEGDFLAEGGGVR 16
||||||||||||||||
Db 1 ADSGEGDFLAEGGGVR 16

Search completed: January 21, 2005, 08:31:10
Job time : 88 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 21, 2005, 08:04:52 ; Search time 26 Seconds
(without alignments)
40.811 Million cell updates/sec

Title: US-09-845-765-1
Perfect score: 83
Sequence: 1 ADSGEGDFLAEGGGVR 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	83	100.0	16	2	US-08-796-598-14	Sequence 14, Appl
2	83	100.0	16	2	US-08-447-175A-14	Sequence 14, Appl
3	83	100.0	16	3	US-08-469-141A-56	Sequence 56, Appl
4	83	100.0	16	4	US-09-525-269A-25	Sequence 25, Appl
5	83	100.0	16	5	PCT-US95-13794-56	Sequence 56, Appl
6	83	100.0	17	4	US-09-845-719B-1	Sequence 1, Appli
7	83	100.0	18	3	US-08-469-141A-55	Sequence 55, Appl
8	83	100.0	18	5	PCT-US95-13794-55	Sequence 55, Appl
9	83	100.0	19	3	US-08-469-141A-54	Sequence 54, Appl
10	83	100.0	19	5	PCT-US95-13794-54	Sequence 54, Appl
11	83	100.0	20	1	US-08-288-657-1	Sequence 1, Appli
12	83	100.0	20	1	US-07-984-884-1	Sequence 1, Appli
13	83	100.0	20	1	US-08-481-810-1	Sequence 1, Appli
14	83	100.0	20	1	US-08-484-426-1	Sequence 1, Appli
15	83	100.0	20	2	US-08-480-818-1	Sequence 1, Appli
16	83	100.0	20	3	US-08-469-141A-53	Sequence 53, Appl
17	83	100.0	20	4	US-09-525-269A-26	Sequence 26, Appl
18	83	100.0	20	5	PCT-US95-13794-53	Sequence 53, Appl
19	83	100.0	21	3	US-08-469-141A-45	Sequence 45, Appl
20	83	100.0	21	5	PCT-US95-13794-45	Sequence 45, Appl
21	83	100.0	22	3	US-08-469-141A-44	Sequence 44, Appl
22	83	100.0	22	3	US-08-469-141A-52	Sequence 52, Appl
23	83	100.0	22	5	PCT-US95-13794-44	Sequence 44, Appl
24	83	100.0	22	5	PCT-US95-13794-52	Sequence 52, Appl
25	83	100.0	23	3	US-08-860-808E-25	Sequence 25, Appl
26	83	100.0	25	3	US-08-440-322-16	Sequence 16, Appl
27	83	100.0	25	3	US-08-440-331-16	Sequence 16, Appl
28	83	100.0	30	2	US-07-963-538B-9	Sequence 9, Appli
29	83	100.0	643	2	US-08-551-356-4	Sequence 4, Appli
30	83	100.0	643	5	PCT-US93-12687-4	Sequence 4, Appli
31	83	100.0	644	1	US-08-206-176-2	Sequence 2, Appli
32	83	100.0	644	4	US-09-919-039-121	Sequence 121, App
33	83	100.0	847	4	US-09-373-157-4	Sequence 4, Appli
34	69	83.1	14	4	US-09-845-725A-1	Sequence 1, Appli
35	63	75.9	17	3	US-08-469-141A-46	Sequence 46, Appl
36	63	75.9	17	5	PCT-US95-13794-46	Sequence 46, Appl
37	58	69.9	12	4	US-09-846-350A-1	Sequence 1, Appli
38	58	69.9	28	6	5196404-16	Patent No. 5196404
39	53	63.9	10	6	5196404-18	Patent No. 5196404
40	53	63.9	10	6	5433940-25	Patent No. 5433940
41	52	62.7	15	3	US-08-469-141A-6	Sequence 6, Appli
42	52	62.7	15	5	PCT-US95-13794-6	Sequence 6, Appli
43	52	62.7	24	2	US-08-978-404B-48	Sequence 48, Appl
44	46	55.4	17	2	US-08-792-553-11	Sequence 11, Appl
45	46	55.4	17	4	US-09-129-192C-45	Sequence 45, Appl

ALIGNMENTS

RESULT 1
US-08-796-598-14
; Sequence 14, Application US/08796598
; Patent No. 5827659
; GENERAL INFORMATION:
; APPLICANT: PATTERSON, DALE H.
; APPLICANT: TARR, GEORGE E.
; TITLE OF INVENTION: METHODS AND APPARATUS FOR SEQUENCING
; TITLE OF INVENTION: POLYMERS USING MASS SPECTROMETRY.
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Administrator - Testa, Hurwitz &
; ADDRESSEE: Thibeault
; STREET: High Street Tower, 125 High Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/796,598
; FILING DATE: 07-FEB-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/446,055
; FILING DATE: 19-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FLYNN Esq., Kerry A.
; REGISTRATION NUMBER: 33,693
; REFERENCE/DOCKET NUMBER: SYP-115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-796-598-14

Query Match 100.0%; Score 83; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ADSGEGDFLAEGGGVR 16
              ||||||||||||||||
Db          1 ADSGEGDFLAEGGGVR 16


RESULT 2
US-08-447-175A-14
; Sequence 14, Application US/08447175A
; Patent No. 5869240
;  GENERAL INFORMATION:
;    APPLICANT:  PATTERSON, DALE H.
;    TITLE OF INVENTION:  METHODS AND APPARATUS FOR SEQUENCING
;    TITLE OF INVENTION:  POLYMERS WITH A STATISTICAL CERTAINTY USING MASS
;    TITLE OF INVENTION:  SPECTROMETRY.
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Patent Administrator - Testa, Hurwitz &
;      ADDRESSEE:  Thibeault, LLP
;      STREET:  High Street Tower, 125 High Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/447,175A
;      FILING DATE:  19-MAY-1995
;      CLASSIFICATION:  422
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  RAUSCHENBACH, Kurt
;      REGISTRATION NUMBER:  40,137
;      REFERENCE/DOCKET NUMBER:  SYP-114
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 248-7000
;      TELEFAX:  (617) 248-7100
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-447-175A-14

  Query Match             100.0%;  Score 83;  DB 2;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-06;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ADSGEGDFLAEGGGVR 16
              ||||||||||||||||
Db          1 ADSGEGDFLAEGGGVR 16


RESULT 3
US-08-469-141A-56
; Sequence 56, Application US/08469141A
; Patent No. 6124107
;  GENERAL INFORMATION:
;    APPLICANT:  MUMFORD, RICHARD A.
;    APPLICANT:  DAVIES, D.T. PHILIP
;    APPLICANT:  DAHLGREN, MARY E.
;    APPLICANT:  BOGER, JOSHUA S.
;    APPLICANT:  HUMES, JOHN L.
;    TITLE OF INVENTION:  ASSAY FOR MARKER OF HUMAN
;    TITLE OF INVENTION:  POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY
;    NUMBER OF SEQUENCES:  71
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DR. CHRISTINE E. CARTY
;      STREET:  126 E. LINCOLN AVENUE., P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07065-0907
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/469,141A
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CARTY, CHRISTINE E.
;      REGISTRATION NUMBER:  36,099
;      REFERENCE/DOCKET NUMBER:  17461IB
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908)-594-6734
;      TELEFAX:  (908)-594-4720
;  INFORMATION FOR SEQ ID NO:  56:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
US-08-469-141A-56

  Query Match             100.0%;  Score 83;  DB 3;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-06;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ADSGEGDFLAEGGGVR 16
              ||||||||||||||||
Db          1 ADSGEGDFLAEGGGVR 16


RESULT 4
US-09-525-269A-25
; Sequence 25, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
;  APPLICANT: Yeaman, Michael R.
;  APPLICANT:  Shen, Alexander J.
;  TITLE OF INVENTION: Antimicrobial Peptides and Derived
;  TITLE OF INVENTION:  Metapeptides
;  FILE REFERENCE: 66742-025(HR5614)
;  CURRENT APPLICATION NUMBER: US/09/525,269A
;  CURRENT FILING DATE:  2000-03-13
;  PRIOR APPLICATION NUMBER: US 09/025,319
;  PRIOR FILING DATE: 1998-02-18
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon
;   OTHER INFORMATION: microbiocidal domains from platelet microbial
;   OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-25

  Query Match             100.0%;  Score 83;  DB 4;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-06;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ADSGEGDFLAEGGGVR 16
              ||||||||||||||||
```

```
Db          1 ADSGEGDFLAEGGGVR 16


RESULT 5
PCT-US95-13794-56
; Sequence 56, Application PC/TUS9513794
;  GENERAL INFORMATION:
;    APPLICANT:  Mumford, Richard A.
;    APPLICANT:  Davies, D.T. Philip
;    APPLICANT:  Dahlgren, Mary E.
;    APPLICANT:  Boger, Joshua S.
;    APPLICANT:  Humes, John L.
;    TITLE OF INVENTION:  ASSAY FOR MARKER OF HUMAN
;    TITLE OF INVENTION:  POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY
;    NUMBER OF SEQUENCES:  71
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dr. Christine E. Carty
;      STREET:  126 E. Lincoln Avenue; P.O. Box 2000
;      CITY:  Rahway
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07065-0907
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/13794
;      FILING DATE:  03-NOV-1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Carty, Christine E.
;      REGISTRATION NUMBER:  36,099
;      REFERENCE/DOCKET NUMBER:  17461IAY
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908) 594-6734
;      TELEFAX:  (908) 594-4720
;  INFORMATION FOR SEQ ID NO:  56:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
PCT-US95-13794-56

  Query Match             100.0%;  Score 83;  DB 5;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-06;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ADSGEGDFLAEGGGVR 16
              ||||||||||||||||
Db          1 ADSGEGDFLAEGGGVR 16


RESULT 6
US-09-845-719B-1
; Sequence 1, Application US/09845719B
; Patent No. 6627606
; GENERAL INFORMATION:
;  APPLICANT: Jackowski, George
;  TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
;  TITLE OF INVENTION:  OF 1465 DALTONS
;  FILE REFERENCE: 2132.035
;  CURRENT APPLICATION NUMBER: US/09/845,719B
;  CURRENT FILING DATE:  2001-04-30
;  NUMBER OF SEQ ID NOS: 1
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 17
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-845-719B-1

  Query Match             100.0%;  Score 83;  DB 4;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4e-06;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ADSGEGDFLAEGGGVR 16
              ||||||||||||||||
Db          1 ADSGEGDFLAEGGGVR 16


RESULT 7
US-08-469-141A-55
; Sequence 55, Application US/08469141A
; Patent No. 6124107
;  GENERAL INFORMATION:
;    APPLICANT:  MUMFORD, RICHARD A.
;    APPLICANT:  DAVIES, D.T. PHILIP
;    APPLICANT:  DAHLGREN, MARY E.
;    APPLICANT:  BOGER, JOSHUA S.
;    APPLICANT:  HUMES, JOHN L.
;    TITLE OF INVENTION:  ASSAY FOR MARKER OF HUMAN
;    TITLE OF INVENTION:  POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY
;    NUMBER OF SEQUENCES:  71
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DR. CHRISTINE E. CARTY
;      STREET:  126 E. LINCOLN AVENUE., P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07065-0907
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/469,141A
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CARTY, CHRISTINE E.
;      REGISTRATION NUMBER:  36,099
;      REFERENCE/DOCKET NUMBER:  17461IB
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908)-594-6734
;      TELEFAX:  (908)-594-4720
;  INFORMATION FOR SEQ ID NO:  55:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
US-08-469-141A-55

  Query Match             100.0%;  Score 83;  DB 3;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-06;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ADSGEGDFLAEGGGVR 16
              ||||||||||||||||
Db          1 ADSGEGDFLAEGGGVR 16


RESULT 8
PCT-US95-13794-55
```

```
; Sequence 55, Application PC/TUS9513794
;  GENERAL INFORMATION:
;    APPLICANT:  Mumford, Richard A.
;    APPLICANT:  Davies, D.T. Philip
;    APPLICANT:  Dahlgren, Mary E.
;    APPLICANT:  Boger, Joshua S.
;    APPLICANT:  Humes, John L.
;    TITLE OF INVENTION:  ASSAY FOR MARKER OF HUMAN
;    TITLE OF INVENTION:  POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY
;    NUMBER OF SEQUENCES:  71
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dr. Christine E. Carty
;      STREET:  126 E. Lincoln Avenue; P.O. Box 2000
;      CITY:  Rahway
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07065-0907
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/13794
;      FILING DATE:  03-NOV-1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Carty, Christine E.
;      REGISTRATION NUMBER:  36,099
;      REFERENCE/DOCKET NUMBER:  17461IAY
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908) 594-6734
;      TELEFAX:  (908) 594-4720
;  INFORMATION FOR SEQ ID NO:  55:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
PCT-US95-13794-55

  Query Match             100.0%;  Score 83;  DB 5;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-06;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ADSGEGDFLAEGGGVR 16
              ||||||||||||||||
Db          1 ADSGEGDFLAEGGGVR 16


RESULT 9
US-08-469-141A-54
; Sequence 54, Application US/08469141A
; Patent No. 6124107
;  GENERAL INFORMATION:
;    APPLICANT:  MUMFORD, RICHARD A.
;    APPLICANT:  DAVIES, D.T. PHILIP
;    APPLICANT:  DAHLGREN, MARY E.
;    APPLICANT:  BOGER, JOSHUA S.
;    APPLICANT:  HUMES, JOHN L.
;    TITLE OF INVENTION:  ASSAY FOR MARKER OF HUMAN
;    TITLE OF INVENTION:  POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY
;    NUMBER OF SEQUENCES:  71
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DR. CHRISTINE E. CARTY
;      STREET:  126 E. LINCOLN AVENUE., P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07065-0907
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/469,141A
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CARTY, CHRISTINE E.
;      REGISTRATION NUMBER:  36,099
;      REFERENCE/DOCKET NUMBER:  17461IB
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908)-594-6734
;      TELEFAX:  (908)-594-4720
;  INFORMATION FOR SEQ ID NO:  54:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
US-08-469-141A-54

  Query Match             100.0%;  Score 83;  DB 3;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-06;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ADSGEGDFLAEGGGVR 16
              ||||||||||||||||
Db          1 ADSGEGDFLAEGGGVR 16


RESULT 10
PCT-US95-13794-54
; Sequence 54, Application PC/TUS9513794
;  GENERAL INFORMATION:
;    APPLICANT:  Mumford, Richard A.
;    APPLICANT:  Davies, D.T. Philip
;    APPLICANT:  Dahlgren, Mary E.
;    APPLICANT:  Boger, Joshua S.
;    APPLICANT:  Humes, John L.
;    TITLE OF INVENTION:  ASSAY FOR MARKER OF HUMAN
;    TITLE OF INVENTION:  POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY
;    NUMBER OF SEQUENCES:  71
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dr. Christine E. Carty
;      STREET:  126 E. Lincoln Avenue; P.O. Box 2000
;      CITY:  Rahway
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07065-0907
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/13794
;      FILING DATE:  03-NOV-1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Carty, Christine E.
;      REGISTRATION NUMBER:  36,099
;      REFERENCE/DOCKET NUMBER:  17461IAY
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908) 594-6734
;      TELEFAX:  (908) 594-4720
```

```
;  INFORMATION FOR SEQ ID NO:  54:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
PCT-US95-13794-54

  Query Match             100.0%;  Score 83;  DB 5;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-06;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ADSGEGDFLAEGGGVR 16
              ||||||||||||||||
Db          1 ADSGEGDFLAEGGGVR 16


RESULT 11
US-08-288-657-1
; Sequence 1, Application US/08288657
; Patent No. 5424291
;  GENERAL INFORMATION:
;    APPLICANT:  Atrash, Butrus
;    APPLICANT:  Jones, David M.
;    APPLICANT:  Szelke, Michael
;    TITLE OF INVENTION:  New Isosteric Peptides
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Richard J. Sterner, Ph.D.
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036-2787
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/288,657
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/751,700
;      FILING DATE:  08-AUG-1991
;      APPLICATION NUMBER:  SE 9102462-0
;      FILING DATE:  28-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sterner Ph.D., Richard J.
;      REGISTRATION NUMBER:  35,372
;      REFERENCE/DOCKET NUMBER:  1103326-871
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-819-8783
;      TELEFAX:  212-354-8113
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  1..20
;      OTHER INFORMATION:  /note= "Peptide sequence containing
;      OTHER INFORMATION:  thrombin cleavage site in the human fibrinogen
;      OTHER INFORMATION:  A-alpha chain."
;    FEATURE:
;      NAME/KEY:  Cleavage-site
;      LOCATION:  16..17
US-08-288-657-1

  Query Match             100.0%;  Score 83;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-06;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ADSGEGDFLAEGGGVR 16
              ||||||||||||||||
Db          1 ADSGEGDFLAEGGGVR 16


RESULT 12
US-07-984-884-1
; Sequence 1, Application US/07984884
; Patent No. 5614499
;  GENERAL INFORMATION:
;    APPLICANT:  Teger-Nilsson, Ann-Catrine E
;    APPLICANT:  Bylund, Ruth E
;    TITLE OF INVENTION:  New peptide derivatives
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  White and Case
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  United States
;      ZIP:  10036-2787
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/984,884
;      FILING DATE:  02-DEC-1992
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sterner, Richard J
;      REGISTRATION NUMBER:  35, 372
;      REFERENCE/DOCKET NUMBER:  1103326-016
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)819-8200
;      TELEFAX:  (212)354-8113
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  N-terminal
US-07-984-884-1

  Query Match             100.0%;  Score 83;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-06;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ADSGEGDFLAEGGGVR 16
              ||||||||||||||||
Db          1 ADSGEGDFLAEGGGVR 16


RESULT 13
US-08-481-810-1
; Sequence 1, Application US/08481810
; Patent No. 5736521
;  GENERAL INFORMATION:
;    APPLICANT:  Teger-Nilsson, Ann-Catrine E
```

```
;    APPLICANT:  Bylund, Ruth E
;    TITLE OF INVENTION:  New peptide derivatives
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  White and Case
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  United States
;      ZIP:  10036-2787
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/481,810
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/984884
;      FILING DATE:  02-DEC-1992
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sterner, Richard J
;      REGISTRATION NUMBER:  35,372
;      REFERENCE/DOCKET NUMBER:  1103326-016
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)819-8200
;      TELEFAX:  (212)354-8113
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  N-terminal
US-08-481-810-1

  Query Match             100.0%;  Score 83;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-06;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ADSGEGDFLAEGGGVR 16
              ||||||||||||||||
Db          1 ADSGEGDFLAEGGGVR 16


RESULT 14
US-08-484-426-1
; Sequence 1, Application US/08484426
; Patent No. 5747460
;  GENERAL INFORMATION:
;    APPLICANT:  Teger-Nilsson, Ann-Catrine E
;    APPLICANT:  Bylund, Ruth E
;    TITLE OF INVENTION:  New peptide derivatives
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  White and Case
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  United States
;      ZIP:  10036-2787
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/484,426
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/984884
;      FILING DATE:  02-DEC-1992
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sterner, Richard J
;      REGISTRATION NUMBER:  35,372
;      REFERENCE/DOCKET NUMBER:  1103326-016
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)819-8200
;      TELEFAX:  (212)354-8113
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  N-terminal
US-08-484-426-1

  Query Match             100.0%;  Score 83;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-06;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ADSGEGDFLAEGGGVR 16
              ||||||||||||||||
Db          1 ADSGEGDFLAEGGGVR 16


RESULT 15
US-08-480-818-1
; Sequence 1, Application US/08480818
; Patent No. 5955433
;  GENERAL INFORMATION:
;    APPLICANT:  Teger-Nilsson, Ann-Catrine E
;    APPLICANT:  Bylund, Ruth E
;    TITLE OF INVENTION:  New peptide derivatives
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  White and Case
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  United States
;      ZIP:  10036-2787
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/480,818
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/984884
;      FILING DATE:  02-DEC-1992
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sterner, Richard J
;      REGISTRATION NUMBER:  35,372
;      REFERENCE/DOCKET NUMBER:  1103326-016
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)819-8200
;      TELEFAX:  (212)354-8113
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
```

; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-480-818-1

  Query Match 100.0%; Score 83; DB 2; Length 20;
  Best Local Similarity 100.0%; Pred. No. 4.8e-06;
  Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSGEGDFLAEGGGVR 16
      ||||||||||||||||
Db 1 ADSGEGDFLAEGGGVR 16

Search completed: January 21, 2005, 08:29:37
Job time : 28 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 21, 2005, 08:04:53 ; Search time 75 Seconds
(without alignments)
77.075 Million cell updates/sec

Title: US-09-845-765-1
Perfect score: 83
Sequence: 1 ADSGEGDFLAEGGGVR 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
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20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	83	100.0	16	9	US-09-846-780-1	Sequence 1, Appli
2	83	100.0	16	9	US-09-826-290-352	Sequence 352, App
3	83	100.0	16	12	US-09-845-765-1	Sequence 1, Appli
4	83	100.0	16	14	US-10-359-363A-2	Sequence 2, Appli
5	83	100.0	16	15	US-10-264-309-8	Sequence 8, Appli
6	83	100.0	16	16	US-10-325-162-1	Sequence 1, Appli
7	83	100.0	16	17	US-10-484-568-60	Sequence 60, Appl
8	83	100.0	17	14	US-10-197-954-53	Sequence 53, Appl
9	83	100.0	24	15	US-10-363-369-3	Sequence 3, Appli
10	83	100.0	24	15	US-10-363-369-4	Sequence 4, Appli
11	83	100.0	24	15	US-10-363-369-5	Sequence 5, Appli
12	83	100.0	24	15	US-10-363-369-6	Sequence 6, Appli
13	83	100.0	24	17	US-10-484-568-1	Sequence 1, Appli
14	83	100.0	24	17	US-10-484-568-3	Sequence 3, Appli
15	83	100.0	24	17	US-10-484-568-10	Sequence 10, Appl
16	83	100.0	24	17	US-10-484-568-25	Sequence 25, Appl
17	83	100.0	24	17	US-10-484-568-40	Sequence 40, Appl
18	83	100.0	24	17	US-10-484-568-41	Sequence 41, Appl
19	83	100.0	24	17	US-10-484-568-42	Sequence 42, Appl
20	83	100.0	24	17	US-10-484-568-43	Sequence 43, Appl
21	83	100.0	24	17	US-10-484-568-44	Sequence 44, Appl
22	83	100.0	24	17	US-10-484-568-45	Sequence 45, Appl
23	83	100.0	24	17	US-10-484-568-46	Sequence 46, Appl
24	83	100.0	24	17	US-10-484-568-47	Sequence 47, Appl
25	83	100.0	24	17	US-10-484-568-48	Sequence 48, Appl
26	83	100.0	24	17	US-10-484-568-49	Sequence 49, Appl
27	83	100.0	25	9	US-09-757-774-16	Sequence 16, Appl
28	83	100.0	28	17	US-10-484-568-61	Sequence 61, Appl
29	83	100.0	28	17	US-10-484-568-62	Sequence 62, Appl
30	83	100.0	78	15	US-10-363-369-15	Sequence 15, Appl
31	83	100.0	360	9	US-09-925-297-587	Sequence 587, App
32	83	100.0	388	15	US-10-236-392-34	Sequence 34, Appl
33	83	100.0	481	15	US-10-236-392-36	Sequence 36, Appl
34	83	100.0	620	10	US-09-931-009A-1	Sequence 1, Appli
35	83	100.0	644	10	US-09-919-039-121	Sequence 121, App
36	83	100.0	644	15	US-10-236-392-32	Sequence 32, Appl
37	83	100.0	847	13	US-10-112-527-4	Sequence 4, Appli
38	80	96.4	16	14	US-10-359-363A-25	Sequence 25, Appl
39	80	96.4	24	17	US-10-484-568-27	Sequence 27, Appl
40	79	95.2	15	9	US-09-845-719A-1	Sequence 1, Appli
41	79	95.2	15	17	US-10-484-568-51	Sequence 51, Appl
42	79	95.2	23	17	US-10-484-568-63	Sequence 63, Appl
43	79	95.2	24	17	US-10-484-568-38	Sequence 38, Appl
44	78	94.0	15	17	US-10-484-568-50	Sequence 50, Appl
45	78	94.0	24	15	US-10-363-369-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-846-780-1
; Sequence 1, Application US/09846780
; Patent No. US20020160423A1
; GENERAL INFORMATION:
; APPLICANT: Jackowski, George
; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
; TITLE OF INVENTION: OF 1536 DALTONS
; FILE REFERENCE: 2132.039
; CURRENT APPLICATION NUMBER: US/09/846,780
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-846-780-1

Query Match 100.0%; Score 83; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSGEGDFLAEGGGVR 16
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Db 1 ADSGEGDFLAEGGGVR 16

RESULT 2
US-09-826-290-352
; Sequence 352, Application US/09826290
; Patent No. US20020164668A1
; GENERAL INFORMATION:
; APPLICANT: Durham, L.Kathryn
; APPLICANT: Friedman, David L.
; APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri

```
;  APPLICANT:  Kimmel, Lida H.
;  APPLICANT:  Parekh, Rajesh Bhikhu
;  APPLICANT:  Potter, David M.
;  APPLICANT:  Rohlff, Christian
;  APPLICANT:  Silber, B. Michael
;  APPLICANT:  Stiger, Thomas R.
;  APPLICANT:  Sunderland, P. Trey
;  APPLICANT:  Townsend, Robert Reid
;  APPLICANT:  White, Frost
;  APPLICANT:  Williams, Stephen A.
;  TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
;  TITLE OF INVENTION:  Uses Therefor, Including Diagnosis and Treatment of
;  TITLE OF INVENTION:  Alzheimer's Disease
;  FILE REFERENCE: 2572-1-001 N2
;  CURRENT APPLICATION NUMBER: US/09/826,290
;  CURRENT FILING DATE:  2001-04-30
;  PRIOR APPLICATION NUMBER: US 60/194,504
;  PRIOR FILING DATE: 2000-04-03
;  PRIOR APPLICATION NUMBER: US 60/253,647
;  PRIOR FILING DATE: 2000-11-28
;  NUMBER OF SEQ ID NOS: 492
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 352
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: homo sapien
US-09-826-290-352

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  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ADSGEGDFLAEGGGVR 16
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Db          1 ADSGEGDFLAEGGGVR 16


RESULT 3
US-09-845-765-1
; Sequence 1, Application US/09845765
; Publication No. US20040198950A1
; GENERAL INFORMATION:
;  APPLICANT: Jackowski, George
;  TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
;  TITLE OF INVENTION:  OF 1518 DALTONS
;  FILE REFERENCE: 2132.036
;  CURRENT APPLICATION NUMBER: US/09/845,765
;  CURRENT FILING DATE:  2001-04-30
;  NUMBER OF SEQ ID NOS: 1
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-845-765-1

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  Best Local Similarity   100.0%;  Pred. No. 1.8e-05;
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Qy          1 ADSGEGDFLAEGGGVR 16
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Db          1 ADSGEGDFLAEGGGVR 16


RESULT 4
US-10-359-363A-2
; Sequence 2, Application US/10359363A
; Publication No. US20030228371A1
; GENERAL INFORMATION:
;  APPLICANT: Skinner, James E.
;  APPLICANT:  Anchin, Jerry M.
;  TITLE OF INVENTION: ANTI-INFARCTION MOLECULES
;  FILE REFERENCE: 22118.0001U4
;  CURRENT APPLICATION NUMBER: US/10/359,363A
;  CURRENT FILING DATE:  2003-02-05
;  PRIOR APPLICATION NUMBER: 60/429,278
;  PRIOR FILING DATE: 2002-11-25
;  PRIOR APPLICATION NUMBER: 60/392,133
;  PRIOR FILING DATE: 2002-06-28
;  PRIOR APPLICATION NUMBER: 60/354,678
;  PRIOR FILING DATE: 2002-02-06
;  NUMBER OF SEQ ID NOS: 104
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/No. US20030228371A1e =
;   OTHER INFORMATION: Synthetic Construct
US-10-359-363A-2

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  Best Local Similarity   100.0%;  Pred. No. 1.8e-05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ADSGEGDFLAEGGGVR 16
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Db          1 ADSGEGDFLAEGGGVR 16


RESULT 5
US-10-264-309-8
; Sequence 8, Application US/10264309
; Publication No. US20040022794A1
; GENERAL INFORMATION:
;  APPLICANT: DURHAM, L. KATHRYN
;  APPLICANT:  FRIEDMAN, DAVID L.
;  APPLICANT:  HERATH, HERATH
;  APPLICANT:  KIMMEL, LIDA H.
;  APPLICANT:  PAREKH, RAJESH B.
;  APPLICANT:  POTTER, DAVID M.
;  APPLICANT:  ROHLFF, CHRISTIAN
;  APPLICANT:  SILBER, B. MICHAEL
;  APPLICANT:  SNYDER, PETER J.
;  APPLICANT:  SOARES, HOLLY D.
;  APPLICANT:  STIGER, THOMAS R.
;  APPLICANT:  SUNDERLAND, P. TREY
;  APPLICANT:  TOWNSEND, ROBERT R.
;  APPLICANT:  WHITE, W. FROST
;  APPLICANT:  WILLIAMS, STEPHEN A.
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR,
;  TITLE OF INVENTION:  INCLUDING DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISEASE
;  FILE REFERENCE: POA-002.01
;  CURRENT APPLICATION NUMBER: US/10/264,309
;  CURRENT FILING DATE:  2002-10-03
;  PRIOR APPLICATION NUMBER: 60/326,708
;  PRIOR FILING DATE: 2001-10-03
;  NUMBER OF SEQ ID NOS: 491
;  SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 8
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-264-309-8

  Query Match             100.0%;  Score 83;  DB 15;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ADSGEGDFLAEGGGVR 16
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Db          1 ADSGEGDFLAEGGGVR 16
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RESULT 6
US-10-325-162-1
; Sequence 1, Application US/10325162
; Publication No. US20040121306A1
; GENERAL INFORMATION:
;  APPLICANT: Kupchak, Peter
;  APPLICANT:  Marshall, John
;  APPLICANT:  Jackowski, George
;  TITLE OF INVENTION: Method of Confirming the Presence of Myocardial Infarction
;  FILE REFERENCE: 2132.132
;  CURRENT APPLICATION NUMBER: US/10/325,162
;  CURRENT FILING DATE:  2002-12-20
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-325-162-1

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Db          1 ADSGEGDFLAEGGGVR 16


RESULT 7
US-10-484-568-60
; Sequence 60, Application US/10484568
; Publication No. US20040248194A1
; GENERAL INFORMATION:
;  APPLICANT: Garcia-Echeverria, Carlos
;  APPLICANT:  Lewis, Claire
;  APPLICANT:  Robinson, Jeffrey
;  TITLE OF INVENTION: Peptide Screen
;  FILE REFERENCE: 4-32520A/32360/361
;  CURRENT APPLICATION NUMBER: US/10/484,568
;  CURRENT FILING DATE:  2004-01-22
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-484-568-60

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  Best Local Similarity   100.0%;  Pred. No. 1.8e-05;
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Qy          1 ADSGEGDFLAEGGGVR 16
              ||||||||||||||||
Db          1 ADSGEGDFLAEGGGVR 16


RESULT 8
US-10-197-954-53
; Sequence 53, Application US/10197954
; Publication No. US20030119021A1
; GENERAL INFORMATION:
;  APPLICANT: K"ster, Hubert
;  APPLICANT:  Siddiqi, Suhaib
;  APPLICANT:  Little, Daniel
;  TITLE OF INVENTION: Capture Compounds, Collections Thereof
;  TITLE OF INVENTION:  And Methods For Analyzing The Proteome And Complex
;  TITLE OF INVENTION:  Compositions
;  FILE REFERENCE: 24743-2305
;  CURRENT APPLICATION NUMBER: US/10/197,954
;  CURRENT FILING DATE:  2002-07-16
;  PRIOR APPLICATION NUMBER: 60/306,019
;  PRIOR FILING DATE: 2001-07-16
;  PRIOR APPLICATION NUMBER: 60/314,123
;  PRIOR FILING DATE: 2001-08-21
;  PRIOR APPLICATION NUMBER: 60/363,433
;  PRIOR FILING DATE: 2002-03-11
;  NUMBER OF SEQ ID NOS: 149
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 53
;   LENGTH: 17
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-197-954-53

  Query Match             100.0%;  Score 83;  DB 14;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ADSGEGDFLAEGGGVR 16
              ||||||||||||||||
Db          2 ADSGEGDFLAEGGGVR 17


RESULT 9
US-10-363-369-3
; Sequence 3, Application US/10363369
; Publication No. US20040039157A1
; GENERAL INFORMATION:
;  APPLICANT: Bioacta Limited
;  TITLE OF INVENTION: Anti-Angiogenic Peptides
;  FILE REFERENCE: P38123WO
;  CURRENT APPLICATION NUMBER: US/10/363,369
;  CURRENT FILING DATE:  2003-06-23
;  PRIOR APPLICATION NUMBER: 0021475.9
;  PRIOR FILING DATE: 2000-09-01
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 24
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-363-369-3

  Query Match             100.0%;  Score 83;  DB 15;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ADSGEGDFLAEGGGVR 16
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Db          1 ADSGEGDFLAEGGGVR 16


RESULT 10
US-10-363-369-4
; Sequence 4, Application US/10363369
; Publication No. US20040039157A1
; GENERAL INFORMATION:
;  APPLICANT: Bioacta Limited
;  TITLE OF INVENTION: Anti-Angiogenic Peptides
;  FILE REFERENCE: P38123WO
;  CURRENT APPLICATION NUMBER: US/10/363,369
;  CURRENT FILING DATE:  2003-06-23
;  PRIOR APPLICATION NUMBER: 0021475.9
;  PRIOR FILING DATE: 2000-09-01
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 24
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (23)..(23)
;   OTHER INFORMATION: any amino acid residue
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US-10-363-369-4

Query Match 100.0%; Score 83; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSGEGDFLAEGGGVR 16
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Db 1 ADSGEGDFLAEGGGVR 16

RESULT 11
US-10-363-369-5
; Sequence 5, Application US/10363369
; Publication No. US20040039157A1
; GENERAL INFORMATION:
; APPLICANT: Bioacta Limited
; TITLE OF INVENTION: Anti-Angiogenic Peptides
; FILE REFERENCE: P38123WO
; CURRENT APPLICATION NUMBER: US/10/363,369
; CURRENT FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: 0021475.9
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (19)..(19)
; OTHER INFORMATION: any amino acid residue
US-10-363-369-5

Query Match 100.0%; Score 83; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSGEGDFLAEGGGVR 16
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Db 1 ADSGEGDFLAEGGGVR 16

RESULT 12
US-10-363-369-6
; Sequence 6, Application US/10363369
; Publication No. US20040039157A1
; GENERAL INFORMATION:
; APPLICANT: Bioacta Limited
; TITLE OF INVENTION: Anti-Angiogenic Peptides
; FILE REFERENCE: P38123WO
; CURRENT APPLICATION NUMBER: US/10/363,369
; CURRENT FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: 0021475.9
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (17)..(17)
; OTHER INFORMATION: any amino acid residue
US-10-363-369-6

Query Match 100.0%; Score 83; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSGEGDFLAEGGGVR 16
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Db 1 ADSGEGDFLAEGGGVR 16

RESULT 13
US-10-484-568-1
; Sequence 1, Application US/10484568
; Publication No. US20040248194A1
; GENERAL INFORMATION:
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Lewis, Claire
; APPLICANT: Robinson, Jeffrey
; TITLE OF INVENTION: Peptide Screen
; FILE REFERENCE: 4-32520A/32360/361
; CURRENT APPLICATION NUMBER: US/10/484,568
; CURRENT FILING DATE: 2004-01-22
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-484-568-1

Query Match 100.0%; Score 83; DB 17; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSGEGDFLAEGGGVR 16
||||||||||||||||
Db 1 ADSGEGDFLAEGGGVR 16

RESULT 14
US-10-484-568-3
; Sequence 3, Application US/10484568
; Publication No. US20040248194A1
; GENERAL INFORMATION:
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Lewis, Claire
; APPLICANT: Robinson, Jeffrey
; TITLE OF INVENTION: Peptide Screen
; FILE REFERENCE: 4-32520A/32360/361
; CURRENT APPLICATION NUMBER: US/10/484,568
; CURRENT FILING DATE: 2004-01-22
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (23)..(23)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (23)..(23)
; OTHER INFORMATION: X = any amino acid
US-10-484-568-3

Query Match 100.0%; Score 83; DB 17; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSGEGDFLAEGGGVR 16
||||||||||||||||
Db 1 ADSGEGDFLAEGGGVR 16

RESULT 15
US-10-484-568-10
; Sequence 10, Application US/10484568

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; Publication No. US20040248194A1
; GENERAL INFORMATION:
;  APPLICANT: Garcia-Echeverria, Carlos
;  APPLICANT:  Lewis, Claire
;  APPLICANT:  Robinson, Jeffrey
;  TITLE OF INVENTION: Peptide Screen
;  FILE REFERENCE: 4-32520A/32360/361
;  CURRENT APPLICATION NUMBER: US/10/484,568
;  CURRENT FILING DATE:  2004-01-22
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;   LENGTH: 24
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   OTHER INFORMATION: X = any amino acid
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (22)..(22)
;   OTHER INFORMATION: X = any amino acid
US-10-484-568-10

  Query Match           100.0%;  Score 83;  DB 17;  Length 24;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ADSGEGDFLAEGGGVR 16
              ||||||||||||||||
Db          1 ADSGEGDFLAEGGGVR 16


Search completed: January 21, 2005, 08:34:36
Job time : 76 secs
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OM protein - protein search, using sw model

Run on: January 21, 2005, 08:04:52 ; Search time 23 Seconds
(without alignments)
66.933 Million cell updates/sec

Title: US-09-845-765-1
Perfect score: 83
Sequence: 1 ADSGEGDFLAEGGGVR 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	83	100.0	644	1	FGHUA	fibrinogen alpha c
2	83	100.0	866	2	D44234	fibrinogen alpha c
3	80	96.4	16	2	A29501	fibrinopeptide A -
4	80	96.4	16	2	B24180	fibrinogen alpha c
5	80	96.4	16	2	A24180	fibrinogen alpha c
6	80	96.4	16	2	B28854	fibrinopeptide A -
7	80	96.4	16	2	C28854	fibrinopeptide A -
8	80	96.4	16	2	A28854	fibrinopeptide A -
9	62	74.7	16	2	H29501	fibrinopeptide A -
10	61	73.5	16	2	G29501	fibrinopeptide A -
11	60	72.3	28	2	A05296	fibrinogen alpha c
12	58	69.9	19	2	B29501	fibrinopeptide A -
13	58	69.9	311	2	A05294	fibrinogen alpha c
14	57	68.7	15	2	F29501	fibrinopeptide A -
15	55	66.3	17	2	E29501	fibrinopeptide A -
16	55	66.3	19	2	C29501	fibrinopeptide A -
17	54	65.1	15	2	I29501	fibrinopeptide A -
18	46	55.4	223	2	B96506	hypothetical prote
19	44	53.0	169	2	G83075	type 4 fimbrial bi
20	44	53.0	274	2	G72685	probable alanyl-tR
21	44	53.0	669	2	A72718	hypothetical prote
22	43	51.8	278	2	S25355	hypothetical prote
23	43	51.8	692	1	S57592	probable phosphoes
24	42.5	51.2	518	2	AI3534	probable binding p
25	42	50.6	15	2	JP0101	fibrinogen alpha c
26	42	50.6	144	2	H84434	probable phloem-sp
27	42	50.6	168	2	T07146	pathogenesis-relat
28	42	50.6	602	1	GEBPT4	gene 10 protein -
29	42	50.6	629	2	B75330	probable ribosomal
30	42	50.6	787	2	A44452	translation initia
31	42	50.6	828	2	G87584	hypothetical prote
32	42	50.6	1024	2	S10056	hemolysin A - Esch
33	41	49.4	21	2	S47200	T-cell receptor J-
34	41	49.4	159	1	VCTO14	pathogenesis-relat
35	41	49.4	159	2	S26238	pathogenesis-relat
36	41	49.4	236	2	S48867	dimethylallyltrans
37	41	49.4	254	2	S30742	hypothetical prote
38	41	49.4	254	2	D86068	hypothetical prote
39	41	49.4	254	2	A91222	hypothetical prote
40	41	49.4	284	2	A97203	2-oxoacid ferredox
41	41	49.4	391	2	T36321	hypothetical prote
42	41	49.4	394	2	AG3616	hypothetical prote
43	41	49.4	399	2	A87392	conserved hypothet
44	41	49.4	425	2	AG2787	long-chain fatty a
45	41	49.4	429	2	A97567	hypothetical prote

ALIGNMENTS

RESULT 1
FGHUA
fibrinogen alpha chain precursor, short splice form [validated] - human
N;Alternate names: coagulation factor I
N;Contains: fibrinopeptide A
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C;Accession: A93956; A43568; A90468; I84456; A44234; C44234; B94433; A90433; B94309; S19
R;Kant, J.A.; Lord, S.T.; Crabtree, G.R.
Proc. Natl. Acad. Sci. U.S.A. 80, 3953-3957, 1983
A;Title: Partial mRNA sequences for human Aalpha, Bbeta, and gamma fibrinogen chains: ev
A;Reference number: A93956; MUID:83247396; PMID:6575389
A;Accession: A93956
A;Molecule type: mRNA
A;Residues: 1-644 <KAN>
A;Cross-references: UNIPROT:P02671; GB:J00128; NID:g182425; PIDN:AAA52427.1; PID:g182426
A;Note: the authors translated the codon GAG for residue 247 as Gly, GGA for residue 438
R;Chung, D.W.; Harris, J.E.; Davie, E.W.
Adv. Exp. Med. Biol. 281, 39-48, 1990
A;Title: Nucleotide sequences of the three genes coding for human fibrinogen.
A;Reference number: A43568; MUID:91344740; PMID:2102623
A;Accession: A43568
A;Molecule type: DNA
A;Residues: 1-330,'A',332-644 <CHU>
A;Cross-references: GB:M64982; NID:g458553; PIDN:AAA17055.1; PID:g458554
R;Rixon, M.W.; Chan, W.Y.; Davie, E.W.; Chung, D.W.
Biochemistry 22, 3237-3244, 1983
A;Title: Characterization of a complementary deoxyribonucleic acid coding for the alpha
A;Reference number: A90468; MUID:83283432; PMID:6688355
A;Accession: A90468
A;Molecule type: mRNA
A;Residues: 1-330,'A',332-629 <RIX>
A;Cross-references: GB:J00127; NID:g182423; PIDN:AAA52426.1; PID:g182424
R;Imam, A.M.A.; Eaton, M.A.W.; Williamson, R.; Humphries, S.
Nucleic Acids Res. 11, 7427-7434, 1983
A;Title: Isolation and characterisation of cDNA clones for the Aalpha- and gamma-chains
A;Reference number: I37393; MUID:84069777; PMID:6689067
A;Accession: I84456
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 110-156 <RES>
A;Cross-references: GB:K02272; NID:g182427; PIDN:AAA52428.1; PID:g182428
R;Fu, Y.; Weissbach, L.; Plant, P.W.; Oddoux, C.; Cao, Y.; Liang, T.J.; Roy, S.N.; Redmar
Biochemistry 31, 11968-11972, 1992
A;Title: Carboxy-terminal-extended variant of the human fibrinogen alpha subunit: a nove
A;Reference number: A44234; MUID:93090725; PMID:1457396
A;Accession: A44234
A;Molecule type: mRNA
A;Residues: 1-51 <FU1>
A;Cross-references: GB:M64982; NID:g458553; PIDN:AAA17055.1; PID:g458554
A;Note: sequence extracted from NCBI backbone (NCBIN:119912, NCBIN:119914, NCBIP:119918)
A;Accession: C44234

A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 605-644 <FU2>
A;Cross-references: GB:M64982; NID:g458553; PIDN:AAA17055.1; PID:g458554
A;Note: sequence extracted from NCBI backbone (NCBIP:119920)
R;Henschen, A.; Lottspeich, F.; Southan, C.; Topfer-Petersen, E.
in Protides of the Biological Fluids, Proc. 28th Colloq., Peeters, H., ed., pp.51-56, Pe
A;Title: Human fibrinogen: sequence, sulfur bridges, glycosylation and some structural v
A;Reference number: A94433
A;Accession: B94433
A;Molecule type: protein
A;Residues: 20-214,'RS',217-298,'G',300-303,'G',305-629 <HEN>
R;Watt, K.W.K.; Cottrell, B.A.; Strong, D.D.; Doolittle, R.F.
Biochemistry 18, 5410-5416, 1979
A;Title: Amino acid sequences studies on the alpha chain of human fibrinogen. Overlappin
A;Reference number: A90433; MUID:80088231; PMID:518846
A;Contents: disulfide bonds
A;Accession: A90433
A;Molecule type: protein
A;Residues: 20-146,'Q',148-195,'N',197-230,'N',232-316,'SG',319-406,'D',408,'N',410-629
R;Blomback, B.; Hessel, B.; Hogg, D.
Thromb. Res. 8, 639-658, 1976
A;Title: Disulfide bridges in NH-2-terminal part of human fibrinogen.
A;Reference number: A94309; MUID:76225080; PMID:936108
A;Contents: variant, and disulfide bonds
A;Accession: B94309
A;Molecule type: protein
A;Residues: 20-65,'T',67-629 <BLO>
R;Dewey, R.S.; Liesch, J.M.; Williams, H.R.; Sugg, E.E.; Dolan, C.A.; Davies, P.; Mumfor
Biochem. J. 281, 519-524, 1992
A;Title: Purification and characterization by fast-atom-bombardment mass spectrometry of
incubation with calcium ionophore A23187.
A;Reference number: S19297; MUID:92143822; PMID:1736899
A;Accession: S19297
A;Molecule type: protein
A;Residues: 20-40 <DEW>
R;Retzios, A.D.; Markland Jr., F.S.
Thromb. Res. 52, 541-552, 1988
A;Title: A direct-acting fibrinolytic enzyme from the venom of Agkistrodon contortrix cc
A;Reference number: A60905; MUID:89162316; PMID:3232124
A;Accession: A60905
A;Molecule type: protein
A;Residues: 433-451 <RET>
R;Fretto, L.J.; Ferguson, E.W.; Steinman, H.M.; McKee, P.A.
J. Biol. Chem. 253, 2184-2195, 1978
A;Title: Localization of the alpha-chain cross-link acceptor sites of human fibrin.
A;Reference number: A92225; MUID:78130085; PMID:632262
A;Contents: annotation; cross-linking acceptor sites
R;Cottrell, B.A.; Strong, D.D.; Watt, K.W.K.; Doolittle, R.F.
Biochemistry 18, 5405-5410, 1979
A;Title: Amino acid sequence studies on the alpha chain of human fibrinogen. Exact locat
A;Reference number: A90432; MUID:80088230; PMID:518845
A;Contents: annotation; cross-linking acceptor sites
R;Henschen, A.; Lottspeich, F.; Kehl, M.; Southan, C.
Ann. N. Y. Acad. Sci. 408, 28-43, 1983
A;Title: Covalent structure of fibrinogen.
A;Reference number: A90037; MUID:83254370; PMID:6575689
A;Contents: annotation; review, disulfide bonds
R;Itarte, E.; Plana, M.; Guasch, M.D.; Martos, C.
Biochem. Biophys. Res. Commun. 117, 631-636, 1983
A;Title: Phosphorylation of fibrinogen by casein kinase 1.
A;Reference number: A90116; MUID:84104274; PMID:6318767
A;Contents: annotation; phosphorylation
A;Note: about one-third of alpha chain molecules in blood were found to be phosphorylate
R;Doolittle, R.F.
Annu. Rev. Biochem. 53, 195-229, 1984
A;Title: Fibrinogen and fibrin.
A;Reference number: A90041; MUID:84305751; PMID:6383194
A;Contents: annotation; review, EM structure, polymerization, ligands
R;Kimura, S.; Aoki, N.
J. Biol. Chem. 261, 15591-15595, 1986
A;Title: Cross-linking site in fibrinogen for alpha-2-plasmin inhibitor.
A;Reference number: A92565; MUID:87057190; PMID:2877981
A;Contents: annotation; cross-linking site for alpha-2-plasmin inhibitor
R;Krishnamurthi, S.; Dickens, T.A.; Patel, Y.; Wheeler-Jones, C.P.D.; Kakkar, V.V.
Biochem. Biophys. Res. Commun. 163, 1256-1264, 1989
A;Title: The fibrinogen-derived peptide (RGDS) prevents proteolytic degradation of prote
A;Reference number: A33261; MUID:89392031; PMID:2783136
A;Contents: annotation; activity of cell attachment (R-G-D) motif
R;Kirschbaum, N.E.; Budzynski, A.Z.
J. Biol. Chem. 265, 13669-13676, 1990
A;Title: A unique proteolytic fragment of human fibrinogen containing the Aalpha COOH-te
A;Reference number: A37117; MUID:90337977; PMID:2143188
A;Contents: annotation; hementin cleavage site
A;Note: hementin, a protease from Haementeria ghilianii, the giant South American leech,
R;Staendker, L.; Sillard, R.; Bensch, K.W.; Ruf, A.; Raida, M.; Schulz-Knappe, P.; Schepk
Biochem. Biophys. Res. Commun. 215, 896-902, 1995
A;Title: In vivo degradation of human fibrinogen A alpha: Detection of cleavage sites anc
A;Reference number: JC4334; MUID:96027996; PMID:7488058
A;Contents: annotation; composition and amino-terminal sequences of carboxyl end peptides
C;Comment: Unlike the beta and gamma chains, the alpha chain is not glycosylated.
C;Comment: The alpha chain binds by 2-4 cross-links to the amino end of fibronectin.
C;Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves
ization sites responsible for the formation of the soft clot.
C;Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabili
ger) and between alpha chains (weaker) of different monomers.
C;Comment: All fibrinogen chains are synthesized in the liver.
C;Comment: See PIR:D44234 for the minor alternative splice form.
C;Genetics:
A;Gene: GDB:FGA
A;Cross-references: GDB:119129; OMIM:134820
A;Map position: 4q28-4q28
A;Introns: 18/3; 60/3; 122/1; 171/2
A;Note: the list of introns is incomplete
C;Complex: The fibrinogen molecule is a hexamer containing two sets of alpha, beta (see F
ins are contained in the core. Two three-chain coiled coils emerge from this core and cor
from the distal domain nodes.
C;Function:
A;Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into f
A;Pathway: blood coagulation
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology
C;Keywords: alternative splicing; blood coagulation; coiled coil; glycoprotein; liver; ph
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-629/Product: fibrinogen alpha chain #status experimental <MAT>
F;20-35/Product: fibrinopeptide A #status experimental <APT>
F;36-629/Product: fibrin alpha chain #status experimental <FGA>
F;36-38/Region: polymerization site, binding to the distal domain of the gamma chain of a
F;57-185/Domain: fibrinogen disulfide ring homology <FDR>
F;591-593/Region: cell attachment (R-G-D) motif
F;22,460/Binding site: phosphate (Ser) (covalent) #status experimental
F;35-36/Cleavage site: Arg-Gly (thrombin) #status experimental
F;47/Disulfide bonds: interchain (to alpha-47) #status experimental
F;55/Disulfide bonds: interchain (to beta-95) #status experimental
F;64/Disulfide bonds: interchain (to gamma-49) #status experimental
F;68/Disulfide bonds: interchain (to beta-106) #status experimental
F;180/Disulfide bonds: interchain (to gamma-165) #status experimental
F;184/Disulfide bonds: interchain (to beta-223) #status experimental
F;288,419/Binding site: carbohydrate (Asn) (covalent) #status absent
F;322/Cross-link: isopeptide (Lys) (interchain to Gln-41 of alpha-2-plasmin inhibitor) #s
F;347,385/Cross-link: isopeptide (Gln) (interchain to Lys N6-amino of alpha) #status expe
F;461-491/Disulfide bonds: #status experimental
F;527,558,575,581,599/Cross-link: isopeptide (Lys) (interchain to Gln of alpha) #status p

Query Match 100.0%; Score 83; DB 1; Length 644;
Best Local Similarity 100.0%; Pred. No. 3.4e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSGEGDFLAEGGGVR 16
||||||||||||||||
Db 20 ADSGEGDFLAEGGGVR 35

RESULT 2
D44234
fibrinogen alpha chain precursor, extended splice form - human
N;Alternate names: coagulation factor I

```
N;Contains: fibrinopeptide A
C;Species: Homo sapiens (man)
C;Date: 10-Jun-1993 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C;Accession: D44234; B44234
R;Fu, Y.; Weissbach, L.; Plant, P.W.; Oddoux, C.; Cao, Y.; Liang, T.J.; Roy, S.N.; Redma
Biochemistry 31, 11968-11972, 1992
A;Title: Carboxy-terminal-extended variant of the human fibrinogen alpha subunit: a nove
A;Reference number: A44234; MUID:93090725; PMID:1457396
A;Accession: D44234
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA; DNA
A;Residues: 1-866 <FU1>
A;Cross-references: UNIPROT:P02671; GB:M58569; NID:g182406; PID:g182407
A;Note: neither the complete nucleic acid sequence nor the complete translation are show
A;Accession: B44234
A;Molecule type: mRNA; DNA
A;Residues: 605-866 <FU2>
A;Note: sequence extracted from NCBI backbone (NCBIP:119917)
C;Comment: The alpha chain binds by 2-4 cross-links to the amino end of fibronectin.
C;Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cleave
ization sites responsible for the formation of the soft clot.
C;Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabili
ger) and between alpha chains (weaker) of different monomers.
C;Comment: All fibrinogen chains are synthesized in the liver.
C;Comment: See PIR:FGHUA for the major splice form. It is not known whether this form is
C;Genetics:
A;Gene: GDB:FGA
A;Cross-references: GDB:119129; OMIM:134820
A;Map position: 4q28-4q28
A;Introns: 18/3; 60/3; 122/1; 171/2
A;Note: the list of introns is incomplete
C;Complex: The fibrinogen molecule is a hexamer containing two sets of three nonidentica
ntained in the core. Two three-chain coiled coils emerge from this core and connect it t
distal domain nodes.
C;Function:
A;Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into
A;Pathway: blood coagulation
C;Superfamily: human extended splice form fibrinogen alpha chain; fibrinogen beta/gamma
C;Keywords: alternative splicing; blood coagulation; glycoprotein; liver; phosphoprotein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-863/Product: fibrinogen alpha chain, extended splice form #status predicted <MAT>
F;20-35/Product: fibrinopeptide A #status experimental <APT>
F;36-863/Product: fibrin alpha chain, extended splice form #status predicted <FGA>
F;57-185/Domain: fibrinogen disulfide ring homology <FDR>
F;591-593/Region: cell attachment (R-G-D) motif
F;629-863/Domain: fibrinogen beta/gamma homology <FBG>
F;22,460/Binding site: phosphate (Ser) (covalent) #status experimental
F;35-36/Cleavage site: Arg-Gly (thrombin) #status experimental
F;47/Disulfide bonds: interchain (to alpha-47) #status experimental
F;55/Disulfide bonds: interchain (to beta-95) #status experimental
F;64/Disulfide bonds: interchain (to gamma-49) #status experimental
F;68/Disulfide bonds: interchain (to beta-106) #status experimental
F;180/Disulfide bonds: interchain (to gamma-165) #status experimental
F;184/Disulfide bonds: interchain (to beta-223) #status experimental
F;288,419/Binding site: carbohydrate (Asn) (covalent) #status absent
F;322/Cross-link: isopeptide (Lys) (interchain to Gln-41 of alpha-2-plasmin inhibitor) #
F;347,385/Cross-link: isopeptide (Gln) (interchain to Lys N6-amino of alpha) #status exp
F;461-491/Disulfide bonds: #status experimental
F;527,558,575,581,599/Cross-link: isopeptide (Lys) (interchain to Gln of alpha) #status
F;686,831/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             100.0%;  Score 83;  DB 2;  Length 866;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ADSGEGDFLAEGGGVR 16
              ||||||||||||||||
Db         20 ADSGEGDFLAEGGGVR 35


RESULT 3
A29501
fibrinopeptide A - baboon
C;Species: Papio sp. (baboon)
C;Date: 21-Nov-1987 #sequence_revision 21-Nov-1987 #text_change 26-Jan-1996
C;Accession: A29501
R;Blombaeck, B.; Blombaeck, M.; Hann, C.
unpublished results, cited by Blombaeck, B., and Blombaeck, M., in Chemotaxonomy and Ser
A;Reference number: A29501
A;Accession: A29501
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-16 <BLO>
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

  Query Match             96.4%;  Score 80;  DB 2;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 2.2e-06;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ADSGEGDFLAEGGGVR 16
              ||:|||||||||||||
Db          1 ADTGEGDFLAEGGGVR 16


RESULT 4
B24180
fibrinogen alpha chain - red guenon (fragment)
N;Contains: fibrinopeptide A
C;Species: Erythrocebus patas (red guenon, hussar)
C;Date: 05-Jun-1988 #sequence_revision 10-Mar-1994 #text_change 09-Jul-2004
C;Accession: B24180
R;Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 97, 1487-1492, 1985
A;Title: Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas monkey (E
uenons, and baboons.
A;Reference number: A91990; MUID:85289140; PMID:3928610
A;Accession: B24180
A;Molecule type: protein
A;Residues: 1-16 <NAK>
A;Cross-references: UNIPROT:P12803
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

  Query Match             96.4%;  Score 80;  DB 2;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 2.2e-06;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ADSGEGDFLAEGGGVR 16
              ||:|||||||||||||
Db          1 ADTGEGDFLAEGGGVR 16


RESULT 5
A24180
fibrinogen alpha chain - Japanese macaque (fragment)
N;Contains: fibrinopeptide A
C;Species: Macaca fuscata (Japanese macaque)
C;Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 09-Jul-2004
C;Accession: A24180
R;Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 97, 1487-1492, 1985
A;Title: Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas monkey (E
uenons, and baboons.
A;Reference number: A91990; MUID:85289140; PMID:3928610
A;Accession: A24180
A;Molecule type: protein
A;Residues: 1-16 <NAK>
A;Cross-references: UNIPROT:P12803
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

  Query Match             96.4%;  Score 80;  DB 2;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 2.2e-06;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ADSGEGDFLAEGGGVR 16
              ||:|||||||||||||
Db          1 ADTGEGDFLAEGGGVR 16
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RESULT 6
B28854
fibrinopeptide A - hamadryas baboon
C;Species: Papio hamadryas (hamadryas baboon)
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004
C;Accession: B28854
R;Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 94, 1973-1978, 1983
A;Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropit
A;Reference number: A91973; MUID:84161822; PMID:6423621
A;Accession: B28854
A;Molecule type: protein
A;Residues: 1-16 <NAK>
A;Cross-references: UNIPROT:P12803
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 96.4%; Score 80; DB 2; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.2e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSGEGDFLAEGGGVR 16
||:|||||||||||||
Db 1 ADTGEGDFLAEGGGVR 16

RESULT 7
C28854
fibrinopeptide A - gelada baboon
C;Species: Theropithecus gelada (gelada baboon)
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004
C;Accession: C28854
R;Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 94, 1973-1978, 1983
A;Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropit
A;Reference number: A91973; MUID:84161822; PMID:6423621
A;Accession: C28854
A;Molecule type: protein
A;Residues: 1-16 <NAK>
A;Cross-references: UNIPROT:P12803
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 96.4%; Score 80; DB 2; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.2e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSGEGDFLAEGGGVR 16
||:|||||||||||||
Db 1 ADTGEGDFLAEGGGVR 16

RESULT 8
A28854
fibrinopeptide A - olive baboon
C;Species: Papio anubis, Papio hamadryas anubis (olive baboon)
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004
C;Accession: A28854
R;Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 94, 1973-1978, 1983
A;Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropit
A;Reference number: A91973; MUID:84161822; PMID:6423621
A;Accession: A28854
A;Molecule type: protein
A;Residues: 1-16 <NAK>
A;Cross-references: UNIPROT:P12803
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 96.4%; Score 80; DB 2; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.2e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSGEGDFLAEGGGVR 16
||:|||||||||||||
Db 1 ADTGEGDFLAEGGGVR 16

RESULT 9
H29501
fibrinopeptide A - gray seal
C;Species: Halichoerus grypus (gray seal)
C;Date: 21-Nov-1987 #sequence_revision 21-Nov-1987 #text_change 09-Jul-2004
C;Accession: H29501
R;Blombaeck, B.; Blombaeck, M.; Hann, C.
unpublished results, cited by Blombaeck, B., and Blombaeck, M., in Chemotaxonomy and Serc
A;Reference number: A29501
A;Accession: H29501
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-16 <BLO>
A;Cross-references: UNIPROT:Q7M3I6
C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfic

Query Match 74.7%; Score 62; DB 2; Length 16;
Best Local Similarity 80.0%; Pred. No. 0.0015;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 DSGEGDFLAEGGGVR 16
|: | ||||||||||
Db 2 DTKESDFLAEGGGVR 16

RESULT 10
G29501
fibrinopeptide A - bear
C;Species: Ursus sp. (bear)
C;Date: 21-Nov-1987 #sequence_revision 08-Jun-1990 #text_change 09-Jul-2004
C;Accession: G29501
R;Blombaeck, B.; Blombaeck, M.; Hann, C.
unpublished results, cited by Blombaeck, B., and Blombaeck, M., in Chemotaxonomy and Serc
A;Reference number: A29501
A;Accession: G29501
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-16 <BLO>
A;Cross-references: UNIPROT:Q7M3I7
C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfic

Query Match 73.5%; Score 61; DB 2; Length 16;
Best Local Similarity 73.3%; Pred. No. 0.0021;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 DSGEGDFLAEGGGVR 16
| ||:|:|||||||
Db 2 DGKEGEFIAEGGGVR 16

RESULT 11
A05296
fibrinogen alpha chain - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C;Accession: A94308; A03118; A37511; A05296; B37511; C03118
R;Birken, S.; Wilner, G.D.; Canfield, R.E.
Thromb. Res. 7, 599-610, 1975
A;Title: Studies of the structure of canine fibrinogen.
A;Reference number: A94308; MUID:76081726; PMID:1198547
A;Accession: A94308
A;Molecule type: protein
A;Residues: 1-28 <BIR>
A;Cross-references: UNIPROT:P02673
R;Blombaeck, B.; Blombaeck, M.; Groendahl, N.J.
Acta Chem. Scand. 19, 1789-1791, 1965
A;Title: Studies on fibrinopeptides from mammals.
A;Reference number: A03118
A;Accession: A03118

A;Molecule type: protein
A;Residues: 1-16 <BLO>
R;Osbahr Jr., A.J.; Colman, R.W.; Laki, K.; Gladner, J.A.
Biochem. Biophys. Res. Commun. 14, 555-558, 1964
A;Reference number: A37511; MUID:66020594; PMID:5836555
A;Accession: A37511
A;Molecule type: protein
A;Residues: 1,'D',3,'EGKQ',8-16 <OSB>
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology
C;Keywords: blood coagulation; liver; phosphoprotein; plasma
F;1-16/Product: fibrinopeptide A #status experimental <APT>
F;3/Binding site: phosphate (Ser) (covalent) (partial) #status experimental

Query Match 72.3%; Score 60; DB 2; Length 28;
Best Local Similarity 73.3%; Pred. No. 0.0055;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 DSGEGDFLAEGGGVR 16
:| ||:|:|||||||
Db 2 NSKEGEFIAEGGGVR 16

RESULT 12
B29501
fibrinopeptide A - European moose
C;Species: Alces alces alces (European moose, elk)
C;Date: 21-Nov-1987 #sequence_revision 21-Nov-1987 #text_change 09-Jul-2004
C;Accession: B29501
R;Blombaeck, B.; Blombaeck, M.; Hann, C.
unpublished results, cited by Blombaeck, B., and Blombaeck, M., in Chemotaxonomy and Ser
A;Reference number: A29501
A;Accession: B29501
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-19 <BLO>
A;Cross-references: UNIPROT:Q7M3I5
C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfi

Query Match 69.9%; Score 58; DB 2; Length 19;
Best Local Similarity 68.8%; Pred. No. 0.0076;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ADSGEGDFLAEGGGVR 16
:| |:||||||||||
Db 4 SDPAGGEFLAEGGGVR 19

RESULT 13
A05294
fibrinogen alpha chain - bovine (fragments)
N;Contains: fibrinopeptide A
C;Species: Bos primigenius taurus (cattle)
C;Date: 05-Jun-1987 #sequence_revision 10-Mar-1994 #text_change 09-Jul-2004
C;Accession: A05294; A25715; A03117; A37505; A37506; A37507; B37505; C03117
R;Henschen, A.; Lottspeich, F.; Topfer-Petersen, E.; Kehl, M.; Timpl, R.
in Protides of the Biological Fluids, Proc. 28th Colloq., ed. Peeters, H., pp.47-50, Per
A;Reference number: A05294
A;Accession: A05294
A;Molecule type: protein
A;Residues: 20-26,'Y',28-49;55-80;81-108 <HEN>
A;Cross-references: UNIPROT:P02672
R;Chung, D.W.; Rixon, M.W.; Davie, E.W.
in Proteins in Biology and Medicine, Bradshaw, R.A., ed., pp.309-328, Academic Press, Ne
A;Title: The biosynthesis of fibrinogen and the cloning of its cDNA.
A;Reference number: A25715
A;Accession: A25715
A;Molecule type: mRNA
A;Residues: 109-311 <CHU>
R;Sjoquist, J.; Blomback, B.; Wallen, P.
Ark. Kemi 16, 425-436, 1960
A;Title: Amino acid sequence of bovine fibrinopeptides.
A;Reference number: A03117
A;Accession: A03117
A;Molecule type: protein
A;Residues: 1-19 <SJO>
R;Folk, J.E.; Gladner, J.A.; Levin, Y.
J. Biol. Chem. 234, 2317-2320, 1959
A;Title: Thrombin-induced formation of co-fibrin. III. Acid degradation studies and summ
A;Reference number: A37505
A;Accession: A37505
A;Molecule type: protein
A;Residues: 1-19 <FOL>
R;Timpl, R.; Pietzek, P.P.; Wachter, E.; van Delden, V.
Biochim. Biophys. Acta 490, 420-429, 1977
A;Title: Disulfide-linked cyanogen bromide peptides of bovine fibrinogen. II. Isolation
A;Reference number: A37506; MUID:77112616; PMID:836881
A;Accession: A37506
A;Molecule type: protein
A;Residues: 20-54 <TIM>
R;Martinelli, R.A.; Inglis, A.S.; Rubira, M.R.; Hageman, T.C.; Hurrell, J.G.R.; Leach, S
Arch. Biochem. Biophys. 192, 27-32, 1979
A;Title: Amino acid sequences of portions of the alpha and beta chains of bovine fibrino
A;Reference number: A37507; MUID:79164394; PMID:434821
A;Accession: A37507
A;Molecule type: protein
A;Residues: 23-52 <MAR>
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology
C;Keywords: blood coagulation; liver; plasma
F;1-19/Product: fibrinopeptide A #status experimental <APT>
F;20-311/Product: fibrinogen alpha chain (fragments) #status experimental <MAT>

Query Match 69.9%; Score 58; DB 2; Length 311;
Best Local Similarity 68.8%; Pred. No. 0.14;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ADSGEGDFLAEGGGVR 16
:| |||| ||||||
Db 4 SDPPSGDFLTEGGGVR 19

RESULT 14
F29501
fibrinopeptide A - wombat
C;Species: Vombatidae gen. sp. (wombat)
C;Date: 21-Nov-1987 #sequence_revision 08-Jun-1990 #text_change 09-Jul-2004
C;Accession: F29501
R;Blombaeck, B.; Blombaeck, M.; Hann, C.
unpublished results, cited by Blombaeck, B., and Blombaeck, M., in Chemotaxonomy and Ser
A;Reference number: A29501
A;Accession: F29501
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <BLO>
A;Cross-references: UNIPROT:Q7M3I8
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 68.7%; Score 57; DB 2; Length 15;
Best Local Similarity 91.7%; Pred. No. 0.0085;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 EGDFLAEGGGVR 16
|| |||||||||
Db 4 EGSFLAEGGGVR 15

RESULT 15
E29501
fibrinopeptide A - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Nov-1987 #sequence_revision 21-Nov-1987 #text_change 09-Jul-2004
C;Accession: E29501
R;Blombaeck, B.; Blombaeck, M.; Hann, C.
unpublished results, cited by Blombaeck, B., and Blombaeck, M., in Chemotaxonomy and Ser
A;Reference number: A29501
A;Accession: E29501
A;Molecule type: protein

A;Residues: 1-17 <BLO>
A;Cross-references: UNIPROT:P14460
R;Blombaeck, B.; Blombaeck, M.; Groendahl, N.J.
Acta Chem. Scand. 19, 1789-1791, 1965
A;Title: Studies on fibrinopeptides from mammals.
A;Reference number: A03118
A;Contents: annotation; confirmation of species assignment
C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfi

Query Match 66.3%; Score 55; DB 2; Length 17;
Best Local Similarity 83.3%; Pred. No. 0.02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy          5 EGDFLAEGGGVR 16
              :|:||||||||| 
Db          6 KGEFLAEGGGVR 17
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Search completed: January 21, 2005, 08:31:39
Job time : 27 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 21, 2005, 08:04:52 ; Search time 91 Seconds
(without alignments)
101.165 Million cell updates/sec

Title: US-09-845-765-1
Perfect score: 83
Sequence: 1 ADSGEGDFLAEGGGVR 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	83	100.0	218	2	Q8WW76	Q8ww76 homo sapien
2	83	100.0	289	2	Q6NSD8	Q6nsd8 homo sapien
3	83	100.0	289	2	AAH70246	Aah70246 homo sapi
4	83	100.0	866	1	FIBA_HUMAN	P02671 homo sapien
5	80	96.4	16	1	FIBA_MACFU	P12803 macaca fusc
6	76	91.6	16	1	FIBA_HYLLA	P14453 hylobates l
7	71	85.5	16	1	FIBA_MANLE	P14455 mandrillus
8	65	78.3	18	1	FIBA_CAMDR	P14444 camelus dro
9	64	77.1	19	1	FIBA_BISBO	P14441 bison bonas
10	62	74.7	15	1	FIBA_SYNCA	P14463 syncerus ca
11	62	74.7	16	1	FIBA_CERSI	P14535 ceratotheri
12	62	74.7	16	2	Q7M3I6	Q7m3i6 halichoerus
13	61	73.5	16	2	Q7M3I7	Q7m3i7 ursus sp. (
14	61	73.5	18	1	FIBA_LAMGL	P14454 lama glama
15	60	72.3	28	1	FIBA_CANFA	P02673 canis famil
16	59	71.1	16	1	FIBA_FELCA	P14450 felis silve
17	59	71.1	16	1	FIBA_TAPTE	P14536 tapirus ter
18	59	71.1	19	1	FIBA_BUBBU	P14442 bubalus bub
19	58	69.9	16	1	FIBA_ODOHE	P14459 odocoileus
20	58	69.9	19	1	FIBA_CEREL	P14446 cervus elap
21	58	69.9	19	2	Q7M3I5	Q7m3i5 alces alces
22	58	69.9	596	1	FIBA_BOVIN	P02672 bos taurus
23	57	68.7	15	2	Q7M3I8	Q7m3i8 vombatidae
24	56	67.5	19	1	FIBA_MUNMU	P14457 muntiacus m
25	55	66.3	17	1	FIBA_PIG	P14460 sus scrofa
26	55	66.3	19	1	FIBA_SHEEP	P14451 ovis aries
27	54	65.1	15	2	Q7M3I9	Q7m3i9 macropus sp
28	54	65.1	16	1	FIBA_EQUAS	P14449 equus asinu
29	54	65.1	19	1	FIBA_CERNI	P14447 cervus nipp
30	53	63.9	14	1	FIBA_HORSE	P14452 equus cabal
31	52	62.7	557	2	Q99K47	Q99k47 mus musculu
32	49	59.0	501	2	Q6UU61	Q6uu61 oryza sativ
33	49	59.0	501	2	AAQ56514	Aaq56514 oryza sat
34	47	56.6	19	1	FIBA_RANTA	P14462 rangifer ta
35	47	56.6	200	2	Q9XFA0	Q9xfa0 ipomoea bat
36	46	55.4	77	2	Q84SA5	Q84sa5 aster tripo
37	46	55.4	223	2	Q9C6Y9	Q9c6y9 arabidopsis
38	46	55.4	286	2	Q6M0G6	Q6m0g6 methanococc
39	46	55.4	286	2	CAF29861	Caf29861 methanoco
40	46	55.4	288	2	Q8U2S7	Q8u2s7 pyrococcus
41	45	54.2	79	2	Q8RUJ7	Q8ruj7 helianthus
42	45	54.2	161	2	Q9AS45	Q9as45 oryza sativ
43	45	54.2	226	2	Q6IL32	Q6il32 drosophila
44	45	54.2	435	2	Q6TFT0	Q6tft0 erwinia amy
45	45	54.2	435	2	Q8GFN7	Q8gfn7 citrobacter

ALIGNMENTS

RESULT 1
Q8WW76
ID Q8WW76 PRELIMINARY; PRT; 218 AA.
AC Q8WW76;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE FGA protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC020764; AAH20764.1; -.
DR HSSP; P02671; 1FZA.
SQ SEQUENCE 218 AA; 24695 MW; 36D756A8116EA94A CRC64;

Query Match 100.0%; Score 83; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ADSGEGDFLAEGGGVR 16
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Db         20 ADSGEGDFLAEGGGVR 35
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RESULT 2
Q6NSD8
ID   Q6NSD8      PRELIMINARY;      PRT;   289 AA.
AC   Q6NSD8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   FGA protein.
GN   Name=FGA;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Strausberg R.;
RL   Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC070246; AAH70246.1; -.
SQ   SEQUENCE   289 AA;  32991 MW;  1CFAECB437F73BA0 CRC64;

  Query Match             100.0%;  Score 83;  DB 2;  Length 289;
  Best Local Similarity   100.0%;  Pred. No. 0.00022;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ADSGEGDFLAEGGGVR 16
              ||||||||||||||||
Db         20 ADSGEGDFLAEGGGVR 35


RESULT 3
AAH70246
ID   AAH70246    PRELIMINARY;      PRT;   289 AA.
AC   AAH70246;
DT   24-MAY-2004 (TrEMBLrel. 27, Created)
DT   24-MAY-2004 (TrEMBLrel. 27, Last sequence update)
DT   24-MAY-2004 (TrEMBLrel. 27, Last annotation update)
DE   FGA protein.
GN   FGA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Strausberg R.;
RL   Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC070246; AAH70246.1; -.
SQ   SEQUENCE   289 AA;  32991 MW;  1CFAECB437F73BA0 CRC64;

  Query Match             100.0%;  Score 83;  DB 2;  Length 289;
  Best Local Similarity   100.0%;  Pred. No. 0.00022;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ADSGEGDFLAEGGGVR 16
              ||||||||||||||||
Db         20 ADSGEGDFLAEGGGVR 35


RESULT 4
FIBA_HUMAN
ID   FIBA_HUMAN     STANDARD;      PRT;   866 AA.
AC   P02671; Q9BX62; Q9UCH2;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Fibrinogen alpha/alpha-E chain precursor [Contains: Fibrinopeptide A].
GN   Name=FGA;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM ALPHA-E).
RX   MEDLINE=93090725; PubMed=1457396;
RA   Fu Y., Weissbach L., Plant P.W., Oddoux C., Cao Y., Liang T.J.,
RA   Roy S.N., Redman C.M., Grieninger G.;
RT   "Carboxy-terminal-extended variant of the human fibrinogen alpha
RT   subunit: a novel exon conferring marked homology to beta and gamma
RT   subunits.";
RL   Biochemistry 31:11968-11972(1992).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM ALPHA-E).
RA   Chung D.W., Grieninger G.;
RT   "Fibrinogen DNA and protein sequences.";
RL   (In) Ebert R.F. (eds.);
RL   Index of variant human fibrinogens, pp.13-24, CRC Press, Boca Raton
RL   (1994).
RN   [3]
RP   SEQUENCE FROM N.A. (ALPHA-E; ALPHA), AND VARIANTS VAL-6; ALA-331 AND
RP   ALA-456.
RA   Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA   Nickerson D.A.;
RT   "SeattleSNPs. NHLBI HL66682 program for genomic applications, UW-
RT   FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
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RP SEQUENCE OF 1-655 FROM N.A. (ISOFORM ALPHA-E).
RC TISSUE=Liver;
RX MEDLINE=91344740; PubMed=2102623;
RA Chung D.W., Harris J.E., Davie E.W.;
RT "Nucleotide sequences of the three genes coding for human
RT fibrinogen.";
RL Adv. Exp. Med. Biol. 281:39-48(1990).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=83247396; PubMed=6575389;
RA Kant J.A., Lord S.T., Crabtree G.R.;
RT "Partial mRNA sequences for human A alpha, B beta, and gamma
RT fibrinogen chains: evolutionary and functional implications.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:3953-3957(1983).
RN [6]
RP SEQUENCE OF 1-629 FROM N.A.
RX MEDLINE=83283432; PubMed=6688355;
RA Rixon M.W., Chan W.-Y., Davie E.W., Chung D.W.;
RT "Characterization of a complementary deoxyribonucleic acid coding for
RT the alpha chain of human fibrinogen.";
RL Biochemistry 22:3237-3244(1983).
RN [7]
RP SEQUENCE OF 20-629.
RA Henschen A., Lottspeich F., Southan C., Topfer-Petersen E.;
RT "Human fibrinogen: sequence, sulfur bridges, glycosylation and some
RT structural variants.";
RL (In) Peeters H. (eds.);
RL Protides of the biological fluids, Proc. 28th colloquium, pp.51-56,
RL Pergamon Press, Oxford (1980).
RN [8]
RP SEQUENCE OF 20-629, AND DISULFIDE BONDS.
RX MEDLINE=80088231; PubMed=518846;
RA Watt K.W.K., Cottrell B.A., Strong D.D., Doolittle R.F.;
RT "Amino acid sequence studies on the alpha chain of human fibrinogen.
RT Overlapping sequences providing the complete sequence.";
RL Biochemistry 18:5410-5416(1979).
RN [9]
RP SEQUENCE OF 110-156 FROM N.A.
RX MEDLINE=84069777; PubMed=6689067;
RA Imam A.M., Eaton M.A., Williamson R., Humphries S.;
RT "Isolation and characterisation of cDNA clones for the A alpha- and
RT gamma-chains of human fibrinogen.";
RL Nucleic Acids Res. 11:7427-7434(1983).
RN [10]
RP SEQUENCE OF 605-644 FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=83254384; PubMed=6575700;
RA Chung D.W., Rixon M.W., Que B.G., Davie E.W.;
RT "Cloning of fibrinogen genes and their cDNA.";
RL Ann. N. Y. Acad. Sci. 408:449-456(1983).
RN [11]
RP SEQUENCE OF 20-35.
RA Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hinton M.;
RT "Studies on fibrinopeptides from primates.";
RL Acta Chem. Scand. 19:1788-1789(1965).
RN [12]
RP CROSS-LINKING ACCEPTOR SITES.
RX MEDLINE=80088230; PubMed=518845;
RA Cottrell B.A., Strong D.D., Watt K.W.K., Doolittle R.F.;
RT "Amino acid sequence studies on the alpha chain of human fibrinogen.
RT Exact location of cross-linking acceptor sites.";
RL Biochemistry 18:5405-5410(1979).
RN [13]
RP CROSS-LINKING ACCEPTOR SITES.
RX MEDLINE=78130085; PubMed=632262;
RA Fretto L.J., Ferguson E.W., Steinman H.M., McKee P.A.;
RT "Localization of the alpha-chain cross-link acceptor sites of human
RT fibrin.";
RL J. Biol. Chem. 253:2184-2195(1978).
RN [14]
RP VARIANT, AND DISULFIDE BONDS.
RX MEDLINE=76225080; PubMed=936108;
RA Blombaeck B., Hessel B., Hogg D.;
RT "Disulfide bridges in NH2-terminal part of human fibrinogen.";
RL Thromb. Res. 8:639-658(1976).
RN [15]
RP REVIEW, EM STRUCTURE, POLYMERIZATION, AND LIGANDS.
RX MEDLINE=84305751; PubMed=6383194;
RA Doolittle R.F.;
RT "Fibrinogen and fibrin.";
RL Annu. Rev. Biochem. 53:195-229(1984).
RN [16]
RP CROSS-LINKING SITE FOR ALPHA-2-PLASMIN INHIBITOR.
RX MEDLINE=87057190; PubMed=2877981;
RA Kimura S., Aoki N.;
RT "Cross-linking site in fibrinogen for alpha 2-plasmin inhibitor.";
RL J. Biol. Chem. 261:15591-15595(1986).
RN [17]
RP PHOSPHORYLATION.
RX MEDLINE=84104274; PubMed=6318767;
RA Itarte E., Plana M., Guasch M.D., Martos C.;
RT "Phosphorylation of fibrinogen by casein kinase 1.";
RL Biochem. Biophys. Res. Commun. 117:631-636(1983).
RN [18]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 26-39.
RX MEDLINE=92218459; PubMed=1560020;
RA Martin P.D., Robertson W., Turk D., Huber R., Bode W., Edwards B.F.P.;
RT "The structure of residues 7-16 of the A alpha-chain of human
RT fibrinogen bound to bovine thrombin at 2.3-A resolution.";
RL J. Biol. Chem. 267:7911-7920(1992).
RN [19]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 130-216.
RX MEDLINE=97472408; PubMed=9333233;
RA Spraggon G., Everse S.J., Doolittle R.F.;
RT "Crystal structures of fragment D from human fibrinogen and its
RT crosslinked counterpart from fibrin.";
RL Nature 389:455-462(1997).
RN [20]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 130-216.
RX MEDLINE=98292395; PubMed=9628725;
RA Everse S.J., Spraggon G., Veerapandian L., Riley M., Doolittle R.F.;
RT "Crystal structure of fragment double-D from human fibrin with two
RT different bound ligands.";
RL Biochemistry 37:8637-8642(1998).
RN [21]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 670-866.
RX MEDLINE=98356117; PubMed=9689040;
RA Spraggon G., Applegate D., Everse S.J., Zhang J.Z., Veerapandian L.,
RA Redman C., Doolittle R.F., Grieninger G.;
RT "Crystal structure of a recombinant alphaEC domain from human
RT fibrinogen-420.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:9099-9104(1998).
RN [22]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=99175089; PubMed=10074346;
RA Everse S.J., Spraggon G., Veerapandian L., Doolittle R.F.;
RT "Conformational changes in fragments D and double-D from human
RT fibrin(ogen) upon binding the peptide ligand Gly-His-Arg-Pro-amide.";
RL Biochemistry 38:2941-2946(1999).
RN [23]
RP VARIANT KYOTO-2.
RX MEDLINE=91300048; PubMed=2070049;
RA Yoshida N., Okuma M., Hirata H., Matsuda M., Yamazumi K., Asakura S.;
RT "Fibrinogen Kyoto II, a new congenitally abnormal molecule,
RT characterized by the replacement of A alpha proline-18 by leucine.";
RL Blood 78:149-153(1991).
RN [24]
RP VARIANT LIMA.
RX MEDLINE=92340680; PubMed=1634621;
RA Maekawa H., Yamazumi K., Muramatsu S., Kaneko M., Hirata H.,
RA Takahashi N., Arocha-Pinango C.L., Rodriguez S., Nagy H.,
RA Perez-Requejo J.L., Matsuda M.;
RT "Fibrinogen Lima: a homozygous dysfibrinogen with an A alpha-arginine-
RT 141 to serine substitution associated with extra N-glycosylation at A
RT alpha-asparagine-139. Impaired fibrin gel formation but normal fibrin-
RT facilitated plasminogen activation catalyzed by tissue-type
RT plasminogen activator.";

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RL   J. Clin. Invest. 90:67-76(1992).
RN   [25]
RP   VARIANT CARACAS-2.
RX   MEDLINE=91268018; PubMed=1675636;
RA   Maekawa H., Yamazumi K., Muramatsu S., Kaneko M., Hirata H.,
RA   Takahashi N., de Bosch N.B., Carvajal Z., Ojeda A.,
RA   Arocha-Pinango C.L., Matsuda M.;
RT   "An A alpha Ser-434 to N-glycosylated Asn substitution in a
RT   dysfibrinogen, fibrinogen Caracas II, characterized by impaired fibrin
RT   gel formation.";
RL   J. Biol. Chem. 266:11575-11581(1991).
RN   [26]
RP   VARIANT DUSART.
RX   MEDLINE=93232289; PubMed=8473507;
RA   Koopman J., Haverkate F., Grimbergen J., Lord S.T., Mosesson M.W.,
RA   Diorio J.P., Siebenlist K.S., Legrand C., Soria J., Soria C.,
RA   Caen J.P.;
RT   "Molecular basis for fibrinogen Dusart (A alpha 554 Arg-->Cys) and its

  Query Match             100.0%;  Score 83;  DB 1;  Length 866;
  Best Local Similarity   100.0%;  Pred. No. 0.00067;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ADSGEGDFLAEGGGVR 16
              ||||||||||||||||
Db         20 ADSGEGDFLAEGGGVR 35


RESULT 5
FIBA_MACFU
ID   FIBA_MACFU     STANDARD;      PRT;    16 AA.
AC   P12803;
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-OCT-1989 (Rel. 12, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN   Name=FGA;
OS   Macaca fuscata fuscata (Japanese macaque),
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey),
OS   Macaca mulatta (Rhesus macaque),
OS   Cercopithecus aethiops (Green monkey) (Grivet),
OS   Erythrocebus patas (Red guenon) (Cercopithecus patas),
OS   Papio anubis (Olive baboon),
OS   Papio hamadryas (Hamadryas baboon), and
OS   Theropithecus gelada (Gelada baboon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9543, 9541, 9544, 9534, 9538, 9555, 9557, 9565;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=E.patas, and M.fuscata;
RX   MEDLINE=85289140; PubMed=3928610;
RA   Nakamura S., Takenaka O., Takahashi K.;
RT   "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas
RT   monkey (Erythrocebus patas): their amino acid sequences, restricted
RT   mutations, and a molecular phylogeny for macaques, guenons, and
RT   baboons.";
RL   J. Biochem. 97:1487-1492(1985).
RN   [2]
RP   SEQUENCE.
RC   SPECIES=P.anubis, P.hamadryas, and T.gelada;
RX   MEDLINE=84161822; PubMed=6423621;
RA   Nakamura S., Takenaka O., Takahashi K.;
RT   "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
RT   and Theropithecus gelada): their amino acid sequences and evolutionary
RT   rates and a molecular phylogeny for the baboons.";
RL   J. Biochem. 94:1973-1978(1983).
RN   [3]
RP   SEQUENCE.
RC   SPECIES=C.aethiops, M.mulatta, and M.fascicularis;
RA   Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hinton M.;
RT   "Studies on fibrinopeptides from primates.";
RL   Acta Chem. Scand. 19:1788-1789(1965).
CC   -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC       polymerize into fibrin and acting as a cofactor in platelet
CC       aggregation.
CC   -!- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains
CC       (alpha, beta and gamma), linked to each other by disulfide bonds.
CC   -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC       which cleaves fibrinopeptides A and B from alpha and beta chains,
CC       and thus exposes the N-terminal polymerization sites responsible
CC       for the formation of the soft clot.
DR   PIR; A24180; A24180.
DR   PIR; A28854; A28854.
DR   PIR; B24180; B24180.
DR   PIR; B28854; B28854.
DR   PIR; C28854; C28854.
KW   Blood coagulation; Direct protein sequencing; Plasma.
FT   PEPTIDE       1     16       Fibrinopeptide A.
FT   NON_TER      16     16
SQ   SEQUENCE   16 AA;  1551 MW;  49E8CBB63EA04DD3 CRC64;

  Query Match             96.4%;  Score 80;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 3.5e-05;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ADSGEGDFLAEGGGVR 16
              ||:|||||||||||||
Db          1 ADTGEGDFLAEGGGVR 16


RESULT 6
FIBA_HYLLA
ID   FIBA_HYLLA     STANDARD;      PRT;    16 AA.
AC   P14453;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN   Name=FGA;
OS   Hylobates lar (Common gibbon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX   NCBI_TaxID=9580;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=70294424; PubMed=5466708;
RA   Mross G.A., Doolittle R.F., Roberts B.F.;
RT   "Gibbon fibrinopeptides: identification of a glycine-serine allelism
RT   at position B-3.";
RL   Science 170:468-470(1970).
CC   -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC       polymerize into fibrin and acting as a cofactor in platelet
CC       aggregation.
CC   -!- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains
CC       (alpha, beta and gamma), linked to each other by disulfide bonds.
CC   -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC       which cleaves fibrinopeptides A and B from alpha and beta chains,
CC       and thus exposes the N-terminal polymerization sites responsible
CC       for the formation of the soft clot.
KW   Blood coagulation; Direct protein sequencing; Plasma.
FT   PEPTIDE       1     16       Fibrinopeptide A.
FT   NON_TER      16     16
SQ   SEQUENCE   16 AA;  1565 MW;  49E98EB63EA04DD3 CRC64;

  Query Match             91.6%;  Score 76;  DB 1;  Length 16;
  Best Local Similarity   87.5%;  Pred. No. 0.00014;
  Matches   14;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ADSGEGDFLAEGGGVR 16
              ||:|||:|||||||||
Db          1 ADTGEGEFLAEGGGVR 16


RESULT 7
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FIBA_MANLE
ID   FIBA_MANLE     STANDARD;      PRT;    16 AA.
AC   P14455;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN   Name=FGA;
OS   Mandrillus leucophaeus (Drill) (Papio leucophaeus).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Mandrillus.
OX   NCBI_TaxID=9568;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=69115139; PubMed=4974768;
RA   Doolittle R.F., Glascow C., Mross G.A.;
RT   "Characterization of fibrinopeptides A and B from a drill (Mandrillus
RT   leucophaeus).";
RL   Biochim. Biophys. Acta 175:217-219(1969).
CC   -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC       polymerize into fibrin and acting as a cofactor in platelet
CC       aggregation.
CC   -!- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains
CC       (alpha, beta and gamma), linked to each other by disulfide bonds.
CC   -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC       which cleaves fibrinopeptides A and B from alpha and beta chains,
CC       and thus exposes the N-terminal polymerization sites responsible
CC       for the formation of the soft clot.
KW   Blood coagulation; Direct protein sequencing; Plasma.
FT   PEPTIDE       1     16       Fibrinopeptide A.
FT   NON_TER      16     16
SQ   SEQUENCE   16 AA;  1567 MW;  08E8CBB77BA051A4 CRC64;

  Query Match             85.5%;  Score 71;  DB 1;  Length 16;
  Best Local Similarity   75.0%;  Pred. No. 0.00082;
  Matches   12;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ADSGEGDFLAEGGGVR 16
              ||:|:|||: ||||||
Db          1 ADTGDGDFITEGGGVR 16


RESULT 8
FIBA_CAMDR
ID   FIBA_CAMDR     STANDARD;      PRT;    18 AA.
AC   P14444;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN   Name=FGA;
OS   Camelus dromedarius (Dromedary) (Arabian camel).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX   NCBI_TaxID=9838;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=67209145; PubMed=6033721;
RA   Doolittle R.F., Schubert D., Schwartz S.A.;
RT   "Amino acid sequence studies on artiodactyl fibrinopeptides. I.
RT   Dromedary camel, mule deer, and cape buffalo.";
RL   Arch. Biochem. Biophys. 118:456-467(1967).
CC   -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC       polymerize into fibrin and acting as a cofactor in platelet
CC       aggregation.
CC   -!- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains
CC       (alpha, beta and gamma), linked to each other by disulfide bonds.
CC   -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC       which cleaves fibrinopeptides A and B from alpha and beta chains,
CC       and thus exposes the N-terminal polymerization sites responsible
CC       for the formation of the soft clot.
KW   Blood coagulation; Direct protein sequencing; Plasma.
FT   PEPTIDE       1     18       Fibrinopeptide A.
FT   NON_TER      18     18
SQ   SEQUENCE   18 AA;  1835 MW;  244448763D7F4CC6 CRC64;

  Query Match             78.3%;  Score 65;  DB 1;  Length 18;
  Best Local Similarity   80.0%;  Pred. No. 0.0076;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 DSGEGDFLAEGGGVR 16
              |: ||:|||||||||
Db          4 DADEGEFLAEGGGVR 18


RESULT 9
FIBA_BISBO
ID   FIBA_BISBO     STANDARD;      PRT;    19 AA.
AC   P14441;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN   Name=FGA;
OS   Bison bonasus (European bison).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Bovinae; Bison.
OX   NCBI_TaxID=9902;
RN   [1]
RP   SEQUENCE.
RA   Blomback B., Blomback M., Grondahl N.J.;
RT   "Studies on fibrinopeptides from mammals.";
RL   Acta Chem. Scand. 19:1789-1791(1965).
CC   -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC       polymerize into fibrin and acting as a cofactor in platelet
CC       aggregation.
CC   -!- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains
CC       (alpha, beta and gamma), linked to each other by disulfide bonds.
CC   -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC       which cleaves fibrinopeptides A and B from alpha and beta chains,
CC       and thus exposes the N-terminal polymerization sites responsible
CC       for the formation of the soft clot.
KW   Blood coagulation; Direct protein sequencing; Plasma.
FT   PEPTIDE       1     19       Fibrinopeptide A.
FT   NON_TER      19     19
SQ   SEQUENCE   19 AA;  1836 MW;  9BA55A0F473B59C5 CRC64;

  Query Match             77.1%;  Score 64;  DB 1;  Length 19;
  Best Local Similarity   75.0%;  Pred. No. 0.011;
  Matches   12;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ADSGEGDFLAEGGGVR 16
              :|   ||||||||||
Db          4 SDPASGDFLAEGGGVR 19


RESULT 10
FIBA_SYNCA
ID   FIBA_SYNCA     STANDARD;      PRT;    15 AA.
AC   P14463;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN   Name=FGA;
OS   Syncerus caffer (Cape buffalo).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Bovinae; Syncerus.
OX   NCBI_TaxID=9970;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=67209145; PubMed=6033721;
RA   Doolittle R.F., Schubert D., Schwartz S.A.;
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RT   "Amino acid sequence studies on artiodactyl fibrinopeptides. I.
RT   Dromedary camel, mule deer, and cape buffalo.";
RL   Arch. Biochem. Biophys. 118:456-467(1967).
CC   -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC       polymerize into fibrin and acting as a cofactor in platelet
CC       aggregation.
CC   -!- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains
CC       (alpha, beta and gamma), linked to each other by disulfide bonds.
CC   -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC       which cleaves fibrinopeptides A and B from alpha and beta chains,
CC       and thus exposes the N-terminal polymerization sites responsible
CC       for the formation of the soft clot.
KW   Blood coagulation; Direct protein sequencing; Plasma.
FT   PEPTIDE       1     15       Fibrinopeptide A.
FT   NON_TER      15     15
SQ   SEQUENCE   15 AA;  1480 MW;  4E998EA5F0B41CC6 CRC64;

  Query Match             74.7%;  Score 62;  DB 1;  Length 15;
  Best Local Similarity   73.3%;  Pred. No. 0.018;
  Matches   11;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 DSGEGDFLAEGGGVR 16
              : | |:|||||||||
Db          1 EDGSGEFLAEGGGVR 15


RESULT 11
FIBA_CERSI
ID   FIBA_CERSI     STANDARD;      PRT;    16 AA.
AC   P14535;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN   Name=FGA;
OS   Ceratotherium simum (White rhinoceros) (Square-lipped rhinoceros).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Ceratotherium.
OX   NCBI_TaxID=9807;
RN   [1]
RP   SEQUENCE.
RA   O'Neil P.B., Doolittle R.F.;
RT   "Mammalian phylogeny based on fibrinopeptide amino acid sequences.";
RL   Syst. Zool. 22:590-595(1973).
CC   -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC       polymerize into fibrin and acting as a cofactor in platelet
CC       aggregation.
CC   -!- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains
CC       (alpha, beta and gamma), linked to each other by disulfide bonds.
CC   -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC       which cleaves fibrinopeptides A and B from alpha and beta chains,
CC       and thus exposes the N-terminal polymerization sites responsible
CC       for the formation of the soft clot.
KW   Blood coagulation; Direct protein sequencing; Plasma.
FT   PEPTIDE       1     16       Fibrinopeptide A.
FT   NON_TER      16     16
SQ   SEQUENCE   16 AA;  1639 MW;  0958CBB6293F4C81 CRC64;

  Query Match             74.7%;  Score 62;  DB 1;  Length 16;
  Best Local Similarity   73.3%;  Pred. No. 0.019;
  Matches   11;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 DSGEGDFLAEGGGVR 16
              :: ||||:|||||||
Db          2 ETTEGDFIAEGGGVR 16


RESULT 12
Q7M3I6
ID   Q7M3I6      PRELIMINARY;      PRT;    16 AA.
AC   Q7M3I6;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Fibrinopeptide A.
OS   Halichoerus grypus (Gray seal).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae; Halichoerus.
OX   NCBI_TaxID=9711;
RN   [1]
RP   SEQUENCE.
RA   Blombaeck B., Blombaeck M., Hann C.;
RL   Unpublished results, cited by:
RL   Blombaeck B., Blombaeck M.;
RL   (In) Hawkes J.G. (eds.);
RL   Chemotaxonomy and Serotaxonomy, pp.0:3-20, Academic Press, New York
RL   (1968).
DR   PIR; H29501; H29501.
SQ   SEQUENCE   16 AA;  1682 MW;  4858DAF2319C4DC3 CRC64;

  Query Match             74.7%;  Score 62;  DB 2;  Length 16;
  Best Local Similarity   80.0%;  Pred. No. 0.019;
  Matches   12;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 DSGEGDFLAEGGGVR 16
              |: | ||||||||||
Db          2 DTKESDFLAEGGGVR 16


RESULT 13
Q7M3I7
ID   Q7M3I7      PRELIMINARY;      PRT;    16 AA.
AC   Q7M3I7;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Fibrinopeptide A.
OS   Ursus sp. (bear).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX   NCBI_TaxID=9641;
RN   [1]
RP   SEQUENCE.
RA   Blombaeck B., Blombaeck M., Hann C.;
RL   Unpublished results, cited by:
RL   Blombaeck B., Blombaeck M.;
RL   (In) Hawkes J.G. (eds.);
RL   Chemotaxonomy and Serotaxonomy, pp.0:3-20, Academic Press, New York
RL   (1968).
DR   PIR; G29501; G29501.
SQ   SEQUENCE   16 AA;  1622 MW;  09598EB6318BD2C4 CRC64;

  Query Match             73.5%;  Score 61;  DB 2;  Length 16;
  Best Local Similarity   73.3%;  Pred. No. 0.027;
  Matches   11;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 DSGEGDFLAEGGGVR 16
              |  ||:|:|||||||
Db          2 DGKEGEFIAEGGGVR 16


RESULT 14
FIBA_LAMGL
ID   FIBA_LAMGL     STANDARD;      PRT;    18 AA.
AC   P14454;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN   Name=FGA;
OS   Lama glama (Llama), and
OS   Lama vicugna (Vicugna) (Vicugna vicugna).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
OX   NCBI_TaxID=9844, 9843;
RN   [1]
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RP   SEQUENCE.
RC   SPECIES=L.glama;
RA   Blomback B., Blomback M., Grondahl N.J.;
RT   "Studies on fibrinopeptides from mammals.";
RL   Acta Chem. Scand. 19:1789-1791(1965).
RN   [2]
RP   SEQUENCE.
RC   SPECIES=L.vicugna;
RA   Mross G.A., Doolittle R.F.;
RT   "Amino acid sequence studies on artiodacty fibrinopeptides.";
RL   Arch. Biochem. Biophys. 122:674-684(1967).
CC   -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC       polymerize into fibrin and acting as a cofactor in platelet
CC       aggregation.
CC   -!- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains
CC       (alpha, beta and gamma), linked to each other by disulfide bonds.
CC   -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC       which cleaves fibrinopeptides A and B from alpha and beta chains,
CC       and thus exposes the N-terminal polymerization sites responsible
CC       for the formation of the soft clot.
KW   Blood coagulation; Direct protein sequencing; Plasma.
FT   PEPTIDE       1     18       Fibrinopeptide A.
FT   NON_TER      18     18
SQ   SEQUENCE   18 AA;  1834 MW;  2444487B8B7F4CC6 CRC64;

  Query Match             73.5%;  Score 61;  DB 1;  Length 18;
  Best Local Similarity   73.3%;  Pred. No. 0.031;
  Matches   11;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 DSGEGDFLAEGGGVR 16
              |: :|:|||||||||
Db          4 DADKGEFLAEGGGVR 18


RESULT 15
FIBA_CANFA
ID   FIBA_CANFA     STANDARD;      PRT;    28 AA.
AC   P02673; P14464;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN   Name=FGA;
OS   Canis familiaris (Dog), and
OS   Vulpes vulpes (Red fox).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615, 9627;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=C.familiaris;
RX   MEDLINE=76081726; PubMed=1198547;
RA   Birken S., Wilner G.D., Canfield R.E.;
RT   "Studies of the structure of canine fibrinogen.";
RL   Thromb. Res. 7:599-610(1975).
RN   [2]
RP   SEQUENCE OF 1-16.
RC   SPECIES=C.familiaris, and V.vulpes;
RA   Blomback B., Blomback M., Grondahl N.J.;
RT   "Studies on fibrinopeptides from mammals.";
RL   Acta Chem. Scand. 19:1789-1791(1965).
RN   [3]
RP   SEQUENCE OF 1-16.
RC   SPECIES=C.familiaris;
RX   MEDLINE=66020594; PubMed=5836555;
RA   Osbahr A.J. Jr., Colman R.W., Laki K., Gladner J.A.;
RT   "The nature of the peptides released from canine fibrinogen.";
RL   Biochem. Biophys. Res. Commun. 14:555-558(1964).
CC   -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC       polymerize into fibrin and acting as a cofactor in platelet
CC       aggregation.
CC   -!- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains
CC       (alpha, beta and gamma), linked to each other by disulfide bonds.
CC   -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC       which cleaves fibrinopeptides A and B from alpha and beta chains,
CC       and thus exposes the N-terminal polymerization sites responsible
CC       for the formation of the soft clot.
DR   PIR; A94308; A05296.
KW   Blood coagulation; Direct protein sequencing; Phosphorylation; Plasma.
FT   PEPTIDE       1     16       Fibrinopeptide A.
FT   MOD_RES       3      3       Phosphoserine (partial).
FT   CONFLICT      2      2       N -> D (in Ref. 2).
FT   CONFLICT      4      7       KEGE -> EGKQ (in Ref. 2).
FT   NON_TER      28     28
SQ   SEQUENCE   28 AA;  2958 MW;  09DCD3F923BFEBD2 CRC64;

  Query Match             72.3%;  Score 60;  DB 1;  Length 28;
  Best Local Similarity   73.3%;  Pred. No. 0.068;
  Matches   11;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 DSGEGDFLAEGGGVR 16
              :| ||:|:|||||||
Db          2 NSKEGEFIAEGGGVR 16


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Job time : 95 secs
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